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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         April 22, 2004, 13:16:25 ; Search time 22 Seconds
                                            (without alignments)
                                            635.938 Million cell updates/sec

Title:          US-10-069-385-1
Perfect score:  1491
Sequence:       1 VAETPTYPWRDAETGERLVC..........RVARMPGLERSVRERFLPVH 271

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:      389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
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                2:  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                  %
Result          Query
  No.    Score  Match Length DB  ID                       Description
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     2    1491  100.0    300  4  US-09-632-277A-2          Sequence 2, Appli
     3    1491  100.0    300  4  US-09-523-323-52          Sequence 52, Appl
     4  1476.5   99.0    299  3  US-09-286-529-17          Sequence 17, Appl
     5    1034   69.3    211  3  US-09-286-529-20          Sequence 20, Appl
     6     855   57.3    146  4  US-09-523-323-59          Sequence 59, Appl
     7     841   56.4    153  3  US-09-286-529-2           Sequence 2, Appli
     8   440.5   29.5    401  3  US-08-974-022-6           Sequence 6, Appli
     9   440.5   29.5    401  3  US-09-042-785A-12         Sequence 12, Appl
    10   440.5   29.5    401  3  US-08-795-445A-6          Sequence 6, Appli
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    38     422   28.3    208  4  US-08-577-788C-50         Sequence 50, Appl
    39     407   27.3    147  4  US-09-527-236A-20         Sequence 20, Appl
    40     407   27.3    147  4  US-09-756-854-20          Sequence 20, Appl
    41     406   27.2    146  4  US-09-523-323-58          Sequence 58, Appl
    42     394   26.4    174  4  US-08-706-945D-136        Sequence 136, App
    43   385.5   25.9    364  4  US-08-706-945D-142        Sequence 142, App
    44   374.5   25.1    364  4  US-08-706-945D-141        Sequence 141, App
    45     373   25.0    139  4  US-08-706-945D-130        Sequence 130, App

                                   ALIGNMENTS

RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
;  GENERAL INFORMATION:
;    APPLICANT:  Emery, John
;    APPLICANT:  Tan, KB
;    APPLICANT:  Truneh, Alem
;    APPLICANT:  Young, Peter
;    TITLE OF INVENTION:  Tumor Necrosis Related Receptor,
;    TITLE OF INVENTION:  TR4
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/794,796
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Han, William T
;      REGISTRATION NUMBER:  34,344
;      REFERENCE/DOCKET NUMBER:  GH50000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5219
;      TELEFAX:  610-270-4026
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  300 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-794-796-2

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  Best Local Similarity   100.0%;  Pred. No. 3.9e-124;
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RESULT 2
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; Sequence 2, Application US/09632277A
; Patent No. 6599716
; GENERAL INFORMATION:
;  APPLICANT: Hsu, Hailing
;  TITLE OF INVENTION: NTR3 A No. 6599716el Member of the TNF-Receptor Supergene Family
;  FILE REFERENCE: 01017/35549A
;  CURRENT APPLICATION NUMBER: US/09/632,277A
;  CURRENT FILING DATE:  2000-08-03
;  PRIOR APPLICATION NUMBER: US 60/147,297
;  PRIOR FILING DATE: 1999-08-04
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-632-277A-2

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Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 3
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; Sequence 52, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT: Ruben, Steven M.
;  APPLICANT: Ullrich, Stephen
;  APPLICANT: Zhai, Yifan
;  TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
;  FILE REFERENCE: 1488.065000C
;  CURRENT APPLICATION NUMBER: US/09/523,323
;  CURRENT FILING DATE: 2000-03-10
;  EARLIER APPLICATION NUMBER: 60/168,380
;  EARLIER FILING DATE: 1999-12-02
;  EARLIER APPLICATION NUMBER: 60/148,326
;  EARLIER FILING DATE: 1999-08-11
;  EARLIER APPLICATION NUMBER: 60/142,657
;  EARLIER FILING DATE: 1999-07-06
;  EARLIER APPLICATION NUMBER: 60/137,457
;  EARLIER FILING DATE: 1999-06-04
;  EARLIER APPLICATION NUMBER: 60/124,041
;  EARLIER FILING DATE: 1999-03-11
;  EARLIER APPLICATION NUMBER: 09/252,656
;  EARLIER FILING DATE: 1999-02-19
;  EARLIER APPLICATION NUMBER: 60/075,409
;  EARLIER FILING DATE: 1998-02-20
;  EARLIER APPLICATION NUMBER: 09/027,287
;  EARLIER FILING DATE: 1998-02-20
;  EARLIER APPLICATION NUMBER: 09/003,886
;  EARLIER FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: 08/822,953
;  EARLIER FILING DATE: 1997-03-21
;  EARLIER APPLICATION NUMBER: 60/013,923
;  EARLIER FILING DATE: 1996-03-22
;  EARLIER APPLICATION NUMBER: 60/030,157
;  EARLIER FILING DATE: 1996-10-31
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-523-323-52

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Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
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Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 4
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
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;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-286-529-17

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; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 20
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-286-529-20

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Qy        181 E 181
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RESULT 6
US-09-523-323-59
; Sequence 59, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT: Ruben, Steven M.
;  APPLICANT: Ullrich, Stephen
;  APPLICANT: Zhai, Yifan
;  TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
;  FILE REFERENCE: 1488.065000C
;  CURRENT APPLICATION NUMBER: US/09/523,323
;  CURRENT FILING DATE: 2000-03-10
;  EARLIER APPLICATION NUMBER: 60/168,380
;  EARLIER FILING DATE: 1999-12-02
;  EARLIER APPLICATION NUMBER: 60/148,326
;  EARLIER FILING DATE: 1999-08-11
;  EARLIER APPLICATION NUMBER: 60/142,657
;  EARLIER FILING DATE: 1999-07-06
;  EARLIER APPLICATION NUMBER: 60/137,457
;  EARLIER FILING DATE: 1999-06-04
;  EARLIER APPLICATION NUMBER: 60/124,041
;  EARLIER FILING DATE: 1999-03-11
;  EARLIER APPLICATION NUMBER: 09/252,656
;  EARLIER FILING DATE: 1999-02-19
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;  EARLIER APPLICATION NUMBER: 09/027,287
;  EARLIER FILING DATE: 1998-02-20
;  EARLIER APPLICATION NUMBER: 09/003,886
;  EARLIER FILING DATE: 1998-01-07
;  EARLIER APPLICATION NUMBER: 08/822,953
;  EARLIER FILING DATE: 1997-03-21
;  EARLIER APPLICATION NUMBER: 60/013,923
;  EARLIER FILING DATE: 1996-03-22
;  EARLIER APPLICATION NUMBER: 60/030,157
;  EARLIER FILING DATE: 1996-10-31
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
;   LENGTH: 146
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-523-323-59

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Db         61 HNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQC 120

Qy        140 QPHRNCTALGLALNVPGSSSHDTLCT 165
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RESULT 7
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
;  APPLICANT:  Catherine Tribouley
;  TITLE OF INVENTION:  NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE:  1408.003/200130.439C1
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;  CURRENT APPLICATION NUMBER: US/09/286,529
;  CURRENT FILING DATE:  1999-04-05
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: human
US-09-286-529-2

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Qy        116 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120

Qy        176 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 208
              |||||||||||||||||||||||||||||||||
Db        121 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 153

RESULT 8
US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-022-6

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209

RESULT 9
US-09-042-785A-12
; Sequence 12, Application US/09042785A
; Patent No. 6194151
;  GENERAL INFORMATION:
;    APPLICANT:  Busfield, Samantha J
;    TITLE OF INVENTION:  NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
;    TITLE OF INVENTION:  AND USES THEREFOR
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,785A
;      FILING DATE:  17-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/938,896
;      FILING DATE:  26-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MEI-001CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-042-785A-12

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
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Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209


RESULT 10
US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-445A-6

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209


RESULT 11
US-08-795-447A-6
; Sequence 6, Application US/08795447A
; Patent No. 6284728
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  Osteoprotegerin
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  One Amgen Center Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91362-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,447A
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378D2
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-447A-6

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209


RESULT 12
US-08-974-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, William J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-186-6

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209

RESULT 13
US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,446B
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  401 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-446B-6

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209

RESULT 14
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
;  APPLICANT: McDonnell, Peter C.
;  APPLICANT: Young, Peter R.
;  APPLICANT: Zou, Jun
;  TITLE OF INVENTION: A Method of Identifying Agonists and
;  TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
;  TITLE OF INVENTION: and TR5
;  FILE REFERENCE: GH50031
;  CURRENT APPLICATION NUMBER: US/09/153,927A
;  CURRENT FILING DATE: 1998-09-16
;  EARLIER APPLICATION NUMBER: 60/061,334
;  EARLIER FILING DATE: 1997-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: Human
US-09-153-927-1

  Query Match             29.5%;  Score 440.5;  DB 3;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202
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Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209


RESULT 15
US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
;  APPLICANT: Michael R. Brigham-Burke
;  APPLICANT:  Peter R. Young
;  TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
;  TITLE OF INVENTION:  ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
;  FILE REFERENCE: GH-50030
;  CURRENT APPLICATION NUMBER: US/09/072,993C
;  CURRENT FILING DATE:  1998-05-06
;  PRIOR APPLICATION NUMBER: 60/055,513
;  PRIOR FILING DATE: 1997-08-13
;  PRIOR APPLICATION NUMBER: 60/056,980
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/057,550
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 401
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-072-993C-1

  Query Match             29.5%;  Score 440.5;  DB 4;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4.3e-31;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db         26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db        146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy        183 ERAVIDF 189
              | |   |
Db        203 EEAFFRF 209

Search completed: April 22, 2004, 13:25:47
Job time : 23 secs
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                     GenCore version 5.1.6
              Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         April 22, 2004, 13:23:50 ; Search time 48 Seconds
                                           (without alignments)
                                           1560.933 Million cell updates/sec

Title:          US-10-069-385-1
Perfect score:  1491
Sequence:       1 VAETPTYPWRDAETGERLVC..........RVARMPGLERSVRERFLPVH 271

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters:      1133595

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA:*
                1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                3:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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                5:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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                7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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    4    1491   100.0    300  9  US-09-935-727-2             Sequence 2, Appli
    5    1491   100.0    300  14  US-10-129-709-3             Sequence 3, Appli
    6    1491   100.0    300  14  US-10-125-985-2             Sequence 2, Appli
    7    1491   100.0    300  14  US-10-310-793-6             Sequence 6, Appli
    8    1491   100.0    300  15  US-10-369-300-19            Sequence 19, Appl
    9    1491   100.0    300  15  US-10-375-680-52            Sequence 52, Appl
   10    1491   100.0    300  15  US-10-418-242-2             Sequence 2, Appli
   11    1491   100.0    300  15  US-10-456-819-1             Sequence 1, Appli
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                                 ALIGNMENTS


RESULT 1
US-10-129-709-1
; Sequence 1, Application US/10129709
; Publication No. US20030055221A1
; GENERAL INFORMATION:
;  APPLICANT: Witcher, Derrick
;  APPLICANT:  Lu, Jirong
;  TITLE OF INVENTION: Improving stability of FLINT through O-linked glycosylation
;  FILE REFERENCE: X-13531M
;  CURRENT APPLICATION NUMBER: US/10/129,709
;  CURRENT FILING DATE:  2002-05-07
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 271
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-129-709-1

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RESULT 2
US-09-896-096A-1
; Sequence 1, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/896,096A
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
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;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-896-096A-1

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RESULT 3
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; Patent No. US20020065210A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/09/894,924
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
;   LENGTH: 300
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;   ORGANISM: Homo sapiens
US-09-894-924-1

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; Sequence 2, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P2
;  CURRENT APPLICATION NUMBER: US/09/935,727
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,270
;  PRIOR FILING DATE: 1999-04-27
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;  PRIOR APPLICATION NUMBER: 60/124,092
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/121,774
;  PRIOR FILING DATE: 1999-03-04
;  PRIOR APPLICATION NUMBER: 09/006,352
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: 60/035,496
;  PRIOR FILING DATE: 1997-01-14
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-935-727-2

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  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 5
US-10-129-709-3
; Sequence 3, Application US/10129709
; Publication No. US20030055221A1
; GENERAL INFORMATION:
;  APPLICANT: Witcher, Derrick
;  APPLICANT:  Lu, Jirong
;  TITLE OF INVENTION: Improving stability of FLINT through O-linked glycosylation
;  FILE REFERENCE: X-13531M
;  CURRENT APPLICATION NUMBER: US/10/129,709
;  CURRENT FILING DATE:  2002-05-07
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
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;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-129-709-3

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RESULT 6
US-10-125-985-2
; Sequence 2, Application US/10125985
; Publication No. US20030166158A1
; GENERAL INFORMATION:
;  APPLICANT: Hsu, Hailing
;  TITLE OF INVENTION: NTR3 A No. US20030166158A1el Member of the TNF-Receptor Supergene
;  TITLE OF INVENTION:  Family
;  FILE REFERENCE: 01017/35549A
;  CURRENT APPLICATION NUMBER: US/10/125,985
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US/09/632,277A
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-125-985-2

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  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 7
US-10-310-793-6
; Sequence 6, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A
;  APPLICANT:  Zhang, Jun
;  APPLICANT:  Wei, Ping
;  TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
;  TITLE OF INVENTION:  Relating To Human Tumor Necrosis Factor-Gamma Beta
;  FILE REFERENCE: PF573
;  CURRENT APPLICATION NUMBER: US/10/310,793
;  CURRENT FILING DATE:  2002-12-06
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;  PRIOR APPLICATION NUMBER: 60/336,695
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 10/226,294
;  PRIOR FILING DATE: 2002-08-23
;  PRIOR APPLICATION NUMBER: 60/314,381
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 09/899,059
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/278,449
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: 60/216,879
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: 09/559,290
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/180,908
;  PRIOR FILING DATE: 2000-02-08
;  PRIOR APPLICATION NUMBER: 60/134,067
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/132,227
;  PRIOR FILING DATE: 1999-05-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.1
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;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: human
US-10-310-793-6

  Query Match             100.0%;  Score 1491;  DB 14;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-116;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 8
US-10-369-300-19
; Sequence 19, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
;  APPLICANT: Fraser, Christopher
;  APPLICANT:  Hancock, Wayne
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
;  TITLE OF INVENTION:  IMMUNE
;  TITLE OF INVENTION:  DISORDERS USING COMBINATION THERAPY
;  FILE REFERENCE: 7853-255
;  CURRENT APPLICATION NUMBER: US/10/369,300
;  CURRENT FILING DATE:  2003-02-19
;  PRIOR APPLICATION NUMBER: 60/358,463
;  PRIOR FILING DATE: 2002-02-19
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 300
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-369-300-19

  Query Match             100.0%;  Score 1491;  DB 15;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-116;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 9
US-10-375-680-52
; Sequence 52, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  APPLICANT:  Yu, Guo-Liang
;  APPLICANT:  Ruben, Steven M
;  APPLICANT:  Ullrich, Stephen
;  APPLICANT:  Zhai, Yifan
;  TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
;  FILE REFERENCE: 1488.065000E
;  CURRENT APPLICATION NUMBER: US/10/375,680
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,234
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-375-680-52

  Query Match             100.0%;  Score 1491;  DB 15;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-116;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
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Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 10
US-10-418-242-2
; Sequence 2, Application US/10418242
; Publication No. US20040013664A1
; GENERAL INFORMATION:
;  APPLICANT: Gentz et al.
;  TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
;  FILE REFERENCE: PF454P3
;  CURRENT APPLICATION NUMBER: US/10/418,242
;  CURRENT FILING DATE:  2003-04-18
;  PRIOR APPLICATION NUMBER: 60/373,604
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: 09/935,727
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/303,224
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/252,131
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: 60/227,598
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: 09/518,931
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/168,235
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: 60/146,371
;  PRIOR FILING DATE: 1999-08-02
;  PRIOR APPLICATION NUMBER: 60/131,964
;  PRIOR FILING DATE: 1999-04-30
;  PRIOR APPLICATION NUMBER: 60/131,279
;  PRIOR FILING DATE: 1999-04-27
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-418-242-2

  Query Match             100.0%;  Score 1491;  DB 15;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-116;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 11
US-10-456-819-1
; Sequence 1, Application US/10456819
; Publication No. US20040014176A1
; GENERAL INFORMATION:
;  APPLICANT: ASHKENAZI, AVI J
;  APPLICANT:  BOTSTEIN, DAVID
;  APPLICANT:  DODGE, KELLY H.
;  APPLICANT:  GURNEY, AUSTIN L.
;  APPLICANT:  KIM, KYUNG JIN
;  APPLICANT:  LAWRENCE, DAVID A.
;  APPLICANT:  PITTI, ROBERT
;  APPLICANT:  ROY, MARGARET A
;  APPLICANT:  TUMAS, DANIEL B
;  APPLICANT:  WOOD, WILLIAM I.
;  TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
;  FILE REFERENCE: P1134R2 REVISED
;  CURRENT APPLICATION NUMBER: US/10/456,819
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: US/09/894,924
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/157,289
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: US 60/059,288
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: US 60/094,640
;  PRIOR FILING DATE: 1998-07-30
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-456-819-1

  Query Match             100.0%;  Score 1491;  DB 15;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-116;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 12
US-10-106-698-4514
; Sequence 4514, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4514
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;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-106-698-4514

  Query Match             100.0%;  Score 1491;  DB 14;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-116;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 130

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 190

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 250

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 310

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        311 GALLVRLLQALRVARMPGLERSVRERFLPVH 341


RESULT 13
US-09-877-156-17
; Sequence 17, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
;  APPLICANT: Catherine Tribouley
;  TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
;  FILE REFERENCE: 1408.003/200130.439C1
;  CURRENT APPLICATION NUMBER: US/09/877,156
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/286,529
;  PRIOR FILING DATE: 1998-04-05
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-877-156-17

  Query Match             99.0%;  Score 1476.5;  DB 9;  Length 299;
  Best Local Similarity   99.6%;  Pred. No. 1.3e-114;
  Matches  270;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSA-SSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 208

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 268

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        269 GALLVRLLQALRVARMPGLERSVRERFLPVH 299
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RESULT 14
US-09-840-795-2
; Sequence 2, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Erin E.
;  APPLICANT:  Mattson, Jeanine D.
;  APPLICANT:  Bates, Elizabeth Esther Mary
;  APPLICANT:  Gorman, Daniel M.
;  APPLICANT:  Lebecque, Serge J.E.
;  TITLE OF INVENTION: Mammalian Genes; Related Reagents
;  FILE REFERENCE: SF0818K
;  CURRENT APPLICATION NUMBER: US/09/840,795
;  CURRENT FILING DATE:  2001-04-23
;  PRIOR APPLICATION NUMBER: 09/351,777
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 300
;   TYPE: PRT
;   ORGANISM: primate
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (79)
;   OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2

  Query Match             98.5%;  Score 1469;  DB 9;  Length 300;
  Best Local Similarity   98.9%;  Pred. No. 5.6e-114;
  Matches  268;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPMTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
               | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 XCYVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 15
US-10-264-049-3112
; Sequence 3112, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA133P1
;  CURRENT APPLICATION NUMBER: US/10/264,049
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/18569
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: US 60/209,467
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 4360
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3112
;   LENGTH: 326
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-049-3112

  Query Match             93.2%;  Score 1389;  DB 15;  Length 326;
  Best Local Similarity   99.6%;  Pred. No. 2.7e-107;
  Matches  251;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 123

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 183

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 243

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 303

Qy        241 GALLVRLLQALR 252
              |||||||||| |
Db        304 GALLVRLLQAAR 315

Search completed: April 22, 2004, 13:30:37
Job time : 49 secs
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                GenCore version 5.1.6
         Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         December  3, 2003, 13:07:01 ; Search time 41 Seconds
                                           (without alignments)
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Title:          US-10-069-385-1
Perfect score:  1491
Sequence:       1 VAETPTYPWRDAETGERLVC..........RVARMPGLERSVRERFLPVH 271

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:      1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result             Query
  No.    Score     Match Length DB  ID                    Description
-----------------------------------------------------------------------------
    1     1491     100.0    271  20  AAY42184             Human mFLINT #1 pr
    2     1491     100.0    271  21  AAB19334             A mature human FAS
    3     1491     100.0    271  21  AAB19705             Human FAS ligand i
    4     1491     100.0    271  21  AAY97247             M68 TNF receptor r
    5     1491     100.0    271  21  AAY96598             Human mature FLINT
    6     1491     100.0    271  22  AAE03567             Human mature fas l
    7     1491     100.0    271  22  AAB68044             Amino acid sequenc
    8     1491     100.0    271  22  AAB68047             Amino acid sequenc
    9     1491     100.0    271  22  AAB74465             Human FLINT mature
   10     1491     100.0    271  23  AAO18767             Human FLINT mature
   11     1491     100.0    271  23  ABB79621             Human Fas ligand i
   12     1491     100.0    271  23  AAE14578             Human mature FLINT
   13     1491     100.0    300  19  AAW66102             Amino acid sequenc
   14     1491     100.0    300  19  AAW63622             Human tumour necro
   15     1491     100.0    300  20  AAY03099             Human lung TNF-rec
   16     1491     100.0    300  20  AAY42182             Human FLINT #1 pro
   17     1491     100.0    300  20  AAY17479             Mammalian tumour n
   18     1491     100.0    300  20  AAY06817             Human DcR3 polypep
   19     1491     100.0    300  20  AAW97749             Human tumour necro
   20     1491     100.0    300  20  AAW95082             Orphan receptor (H
   21     1491     100.0    300  21  AAB19335             A full length huma
   22     1491     100.0    300  21  AAB28559             Human soluble TNF
   23     1491     100.0    300  21  AAB24057             Human PRO212 prote
   24     1491     100.0    300  21  AAB33416             Human PRO212 prote
   25     1491     100.0    300  21  AAB03621             Human Fas ligand i
   26     1491     100.0    300  21  AAY97246             M68 TNF receptor r
   27     1491     100.0    300  21  AAY90357             Human tumour necro
   28     1491     100.0    300  21  AAB24395             Human PRO212 prote
   29     1491     100.0    300  21  AAY96596             Human FLINT.  Homo
   30     1491     100.0    300  22  AAE03568             Human native fas l
   31     1491     100.0    300  22  AAB74466             Human FLINT native
   32     1491     100.0    300  22  AAB71754             Human NTR3.  Homo
   33     1491     100.0    300  22  AAB48161             Human PRO212 polyp
   34     1491     100.0    300  22  AAB50903             Human PRO212 prote
   35     1491     100.0    300  23  AAO18768             Human FLINT protei
   36     1491     100.0    300  23  ABB79622             Human Fas ligand i
   37     1491     100.0    300  23  AAE14579             Human native FLINT
   38     1491     100.0    300  23  AAE20848             Human tumour necro
   39     1491     100.0    341  22  AAG73740             Human colon cancer
   40     1487      99.7    271  21  AAB19709             Protease-resistant
   41     1487      99.7    271  22  AAE03571             Human mature fas l
   42     1487      99.7    271  22  AAB74467             Human FLINT mature
   43     1487      99.7    271  23  AAE14581             Human protease-res
   44     1486      99.7    271  22  AAE03584             Human mature fas l
   45     1486      99.7    271  23  AAE14582             Human protease-res


                              ALIGNMENTS


RESULT 1
AAY42184
ID   AAY42184 standard; Protein; 271 AA.
XX
AC   AAY42184;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human mFLINT #1 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
```

```
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25377.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 31; Fig 3; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human mFLINT.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 20;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 2
AAB19334
ID   AAB19334 standard; Protein; 271 AA.
XX
AC   AAB19334;
XX
DT   19-FEB-2001  (first entry)
XX
DE   A mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW   Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW   tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
```

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KW   acute respiratory distress syndrome; ulcerative colitis;
KW   chronic obstructive pulmonary disease; Crohn's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "optionally replaced with Met"
FT   Misc-difference 2
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 4
FT                   /note= "optionally replaced with Ala"
FT   Misc-difference 12
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 13
FT                   /note= "optionally replaced with Asp or Gln"
FT   Misc-difference 17
FT                   /note= "optionally replaced with Trp"
FT   Misc-difference 25
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 34
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 35
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 36
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 37
FT                   /note= "optionally replaced with Asn or Thr"
FT   Misc-difference 38
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 53
FT                   /note= "optionally replaced with Asp"
FT   Misc-difference 63
FT                   /note= "optionally replaced with Trp"
FT   Misc-difference 67
FT                   /note= "optionally replaced with Asp"
FT   Misc-difference 69
FT                   /note= "optionally replaced with Glu"
FT   Misc-difference 75
FT                   /note= "optionally replaced with Pro"
FT   Misc-difference 82
FT                   /note= "optionally replaced with Glu or Thr"
FT   Misc-difference 88
FT                   /note= "optionally replaced with Pro"
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FT                   /note= "optionally replaced with Tyr"
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FT                   /note= "optionally replaced with Asp"
FT   Misc-difference 96
FT                   /note= "optionally replaced with Gln"
FT   Misc-difference 101
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 102
FT                   /note= "optionally replaced with Leu"
FT   Misc-difference 104
FT                   /note= "optionally replaced with Ser"
FT   Misc-difference 107
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FT   Misc-difference 114
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FT                   /note= "optionally replaced with Thr"
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FT                   /note= "optionally replaced with Ala"
FT   Misc-difference 166
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FT                   /note= "optionally replaced with Asn"
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FT                   /note= "optionally replaced with Ala"
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FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 172
FT                   /note= "optionally replaced with Asn"
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FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 183
FT                   /note= "optionally replaced with Lys"
FT   Misc-difference 194
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 196
FT                   /note= "optionally replaced with Thr"
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FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 225
FT                   /note= "optionally replaced with Arg"
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FT                   /note= "optionally replaced with Glu"
FT   Misc-difference 270
FT                   /note= "optionally replaced with Gly"
FT
XX
PN   WO200058465-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06417.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140077.
PR   21-JUN-1999;   99US-0140156.
PR   20-OCT-1999;   99US-0160566.
PR   18-FEB-2000; 2000US-0183398.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Becker GW,  Cohen FJ,  Gonzalez-dewhitt PA,  Hale JE,  Micanovic R;
PI   Newton CM,  Noblitt TW,  Rathmachalam R,  Tschang SR,  Witcher DR;
PI   Wroblewski VJ;
XX
DR   WPI; 2000-656167/63.
DR   N-PSDB; AAA75999.
XX
PT   FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT   apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT   chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT   disease  -
XX
PS   Claim 1; Page 112-113; 114pp; English.
XX
CC   The present sequence represents a mature human FAS Ligand Inhibitory
CC   Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC   proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC   FLINT protein is modified to produce analogues, which have greater
CC   potency, longer in vivo half-lives, decreased aggregation, decreased
CC   absorption onto surfaces, increased solubility and improved ease of
CC   formulation. The FLINT analogue is useful for treating a patient
CC   suffering from disease or condition relating to abnormal apoptosis such
CC   as acute lung injury, acute respiratory distress syndrome, pulmonary
CC   fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC   Crohn's disease.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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```
Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
                |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 3
AAB19705
ID   AAB19705 standard; Protein; 271 AA.
XX
AC   AAB19705;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Human FAS ligand inhibitor protein FLINT.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   218..219
FT                   /note= "cleaved by trypsin-like proteases"
FT   Misc-difference 34
FT                   /note= "optionally replaced by Arg, as given in
FT                          Claims 10, 11, 13 and 14"
FT   Misc-difference 36
FT                   /note= "optionally replaced by Thr, as given in
FT                          Claims 10, 11, 13 and 14"
FT   Misc-difference 132
FT                   /note= "optionally replaced by Asn, as given in
FT                          Claim 12"
FT   Misc-difference 194
FT                   /note= "optionally replaced by Asn, as given in
FT                          Claims 11 and 14"
FT   Misc-difference 196
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FT                          Claims 11 and 14"
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FT                          occurring amino acid"
FT   Misc-difference 215
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 216
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid, preferably Pro as
FT                          given in Claims 9 and 15"
FT   Misc-difference 217
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid, preferably Tyr as
FT                          given in Claim 9"
FT   Misc-difference 218
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid, preferably Gln, Glu,
FT                          Ala, Gly, Ser, Val, Tyr or Asn as given in
FT                          Claims, 9, 10, 11, 12, especially Gln as
FT                          given in Claims 13, 14, 15, 35 and 36"
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FT   Misc-difference 219
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 220
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 221
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 222
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
DR   N-PSDB; AAA88730.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases  -
XX
PS   Claim 1; Page 94-95; 100pp; English.
XX
CC   The present sequence is that of human FAS ligand inhibitory protein
CC   FLINT mature protein.  FLINT is a tumour necrosis factor receptor
CC   homologue that binds FAS ligand, preventing its interaction with
CC   FAS.  This interaction is implicated in runaway apoptosis and
CC   inflammatory disease.  FLINT also binds to LIGHT, a membrane-bound
CC   ligand, which may play a role in immune modulation and apoptosis.
CC   The invention relates to novel FLINT analogues (see also AAB19706-09)
CC   that are resistant to proteolysis by trypsin-like proteases between
CC   positions 218 and 219 of the FLINT mature protein sequence.  The
CC   analogues have amino acid substitutions in the region comprising
CC   amino acids 214-222, and may contain additional substitutions at
CC   residues 34, 36, 132, 194 and/or 196.  Nucleic acids, vectors and
CC   transformed host cells for recombinant production of the analogues
CC   are claimed.  FLINT cDNA (see AAA88730) is used as a template for
CC   introducing the required point mutations.  The protease resistant
CC   FLINT analogues are used to prevent or treat acute lung injury,
CC   acute respiratory stress syndrome, ulcerative colitis, chronic
CC   obstructive pulmonary disease, pulmonary fibrosis, to inhibit T
CC   lymphocyte activation, and to facilitate organ preservation for
CC   transplantation (claimed).
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
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Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
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Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 4
AAY97247
ID   AAY97247 standard; Protein; 271 AA.
XX
AC   AAY97247;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein (mature protein).
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
KW   glomerulonephritis; pulmonary fibrosis; heart failure;
KW   atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW   osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW   myocardial infarction; human.
XX
OS   Homo sapiens.
XX
PN   WO200046247-A1.
XX
PD   10-AUG-2000.
XX
PF   04-FEB-2000; 2000WO-US03037.
XX
PR   05-FEB-1999;   99US-0118902.
PR   20-DEC-1999;   99US-0172754.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bai C;
XX
DR   WPI; 2000-506066/45.
XX
PT   Isolated human M68 nucleic acids and proteins which are part of the
PT   tumor necrosis factor receptor (TNFR) family, useful for identifying
PT   modulators that may be used to treat various diseases e.g. cancer,
PT   osteoporosis, Alzheimer's disease
XX
PS   Claim 1; Page 76; 80pp; English.
XX
CC   The M68 protein is a member of a family of proteins which have
CC   roles in immune responses, cell death, cell proliferation and
CC   stimulation of cell differentiation. M68 lacks a transmembrane domain
CC   and is a secreted factor suggesting that it functions as a natural
CC   inhibitor for its ligand. The altered expression pattern of M68 in a
CC   multitude of tissues suggests that M68 may play a role in cancer by
CC   binding to its ligand and blocking apoptotic cell death induced by
CC   such a ligand. This anti-apoptopic role of M68 suggests that
CC   modulators of M68 will be useful in treatment of apoptosis-related
CC   diseases such as various forms of cancer and various bone disorders.
CC   M68 nucleic acids and proteins are therefore useful for treating
CC   conditions involving atypical apoptosis and for identifying
CC   modulators of M68. Modulators of M68 are useful for treatment of
```

```
CC   cancer and other diseases associated with abnormal levels of
CC   apoptosis including systemic lupus erythematosus, Hashimoto's
CC   thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC   diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC   liver diseases, autoimmune gastritis, ulcerative colitis,
CC   glomerulonephritis, pulmonary fibrosis, heart failure,
CC   atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC   osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC   myocardial infarction.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 5
AAY96598
ID   AAY96598 standard; Protein; 271 AA.
XX
AC   AAY96598;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human mature FLINT.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   N-PSDB; AAA51077.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 8; Fig 3; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 6
AAE03567
ID   AAE03567 standard; Protein; 271 AA.
XX
AC   AAE03567;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT).
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   144
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FT                   /note= "N-linked glycosylation site"
FT   Modified-site   174
FT                   /note= "O-linked glycosylation site"
FT   Modified-site   216
FT                   /note= "O-linked glycosylation site"
FT   Cleavage-site   218..219
FT                   /note= "Proteolytic cleavage"
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
DR   N-PSDB; AAD07380.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 1; Page 52-53; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT). FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271

RESULT 7
AAB68044
ID   AAB68044 standard; Protein; 271 AA.
XX
AC   AAB68044;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human mature FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118055-A1.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20807.
XX
PR   10-SEP-1999;   99US-0153339.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273382/28.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions   -
XX
PS   Example 1; Page 39-40; 44pp; English.
XX
CC   The present sequence represents a mature FLINT (FAS Ligand Inhibitory
CC   Protein) polypeptide. The specification describers a composition
CC   comprising a divalent metal cation and FLINT protein. The composition
CC   is used either for reducing, reversing or eliminating aggregation and
CC   precipitation of FLINT or for inducing oligomerisation or aggregation
CC   of FLINT molecules. They can be used for purifying FLINT and/or
CC   maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 8
AAB68047
ID   AAB68047 standard; Protein; 271 AA.
XX
AC   AAB68047;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human mature FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118041-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20805.
XX
PR   10-SEP-1999;   99US-0153445.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273381/28.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions  -
XX
PS   Disclosure; Page 30-31; 33pp; English.
XX
CC   The present sequence represents a human mature FLINT (FAS Ligand
CC   Inhibitory Protein) polypeptide. The specification describes a
CC   composition comprising a divalent metal cation and FLINT protein. The
CC   composition is used either for reducing, reversing or eliminating
CC   aggregation and precipitation of FLINT or for inducing oligomerisation
CC   or aggregation of FLINT molecules. They can be used for purifying FLINT
CC   and/or maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
```

```
Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 9
AAB74465
ID   AAB74465 standard; protein; 271 AA.
XX
AC   AAB74465;
XX
DT   30-MAY-2001  (first entry)
XX
DE   Human FLINT mature protein.
XX
KW   Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW   inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   WO200118202-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20806.
XX
PR   10-SEP-1999;   99US-0153433.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-257796/26.
XX
PT   Compositions useful for reducing/inducing aggregation of a FLINT analog
PT   comprise a divalent metal cation and a protease-resistant FAS Ligand
PT   Inhibitory Protein (FLINT) analog -
XX
PS   Claim 4; Page 41-42; 44pp; English.
XX
CC   The present invention describes a composition comprising a divalent metal
CC   cation associated with a protease resistant Fas ligand inhibitory protein
CC   (FLINT) analogue. The composition is useful in the treatment of diseases
CC   associated with Fas binding to its ligand, such as acute liver failure,
CC   inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC   sequence is the mature FLINT protein.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
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Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 10
AAO18767
ID   AAO18767 standard; Protein; 271 AA.
XX
AC   AAO18767;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Human FLINT mature protein.
XX
KW   Human; FLINT; isoform; glycoprotein; apoptosis; sialic acid;
KW   FAS ligand inhibitory protein; autoimmune disease; inflammatory disease;
KW   infection; ischaemia; cancer; antiinflammatory; immunomodulator;
KW   antibacterial; virucide; vasotropic; neuroprotective; nootropic;
KW   osteopathic; cytostatic; antianaemic; nephrotropic; cardiant;
KW   cardiovascular; hepatotropic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   144
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   174
FT                   /note= "O-linked glycosylation site"
FT   Modified-site   216
FT                   /note= "O-linked glycosylation site"
XX
PN   WO200260947-A2.
XX
PD   08-AUG-2002.
XX
PF   18-JAN-2002; 2002WO-US00509.
XX
PR   01-FEB-2001; 2001US-265690P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Jenkins N,  Witcher DR,  Wroblewski VJ;
XX
DR   WPI; 2002-627468/67.
DR   N-PSDB; AAL48978.
XX
PT   Composition used for treating inflammatory and autoimmune diseases e.g.
PT   graft-versus-host disease, infectious diseases, ischemia and
PT   reperfusion conditions or osteoporosis comprises Fas ligand inhibitory
PT   protein analog isoform -
XX
PS   Example 1; Page 41-42; 47pp; English.
XX
CC   The present invention relates to a composition comprising a Fas ligand
CC   inhibitory protein (FLINT) analogue isoform. The analogue comprises a
CC   FLINT protein where a change in the sequence results in an additional
CC   glycosylation site. The composition has an average sialic acid content of
CC   0.5-9.5 sialic acids per molecule of FLINT. The composition can be used
CC   for regulating apoptosis and for treating or preventing inflammatory and
CC   autoimmune diseases (particularly rheumatoid arthritis, inflammatory
CC   bowel disease, graft-versus-host disease, insulin-dependent diabetes,
CC   pancreatitis, psoriasis, multiple sclerosis, Grave's disease, transplant
CC   rejection, autoimmune gastritis or fibrosing lung disease), infectious
CC   diseases (particularly HIV-induced lymphopenia, fulminant viral hepatitis
CC   B/C or chronic hepatitis/cirrhosis), ischaemia and reperfusion conditions
CC   (particularly acute coronary syndrome, acute myocardial infarction,
CC   congestive heart failure, acute cerebral ischaemia/infarction or
CC   brain/spinal cord trauma), Alzheimer's disease, chronic
CC   glomerulonephritis, osteoporosis, aplastic anaemia, myelodysplasia, or
CC   chronic obstructive pulmonary disease (COPD). The composition is also
CC   useful for cytoprotection during cancer treatment or as an adjuvant to
CC   chemotherapy. The present sequence is the human FLINT mature protein.
```

```
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 23;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 11
ABB79621
ID   ABB79621 standard; Protein; 271 AA.
XX
AC   ABB79621;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human Fas ligand inhibitory protein (FLINT) mature polypeptide.
XX
KW   Fas ligand inhibitory protein; FLINT; human; apoptosis;
KW   antirheumatic; antiarthritic; immunosuppressive; antidiabetic;
KW   antibacterial; antiinflammatory; thyromimetic; antithyroid;
KW   dermatological; hepatotropic; virucide; cardiant; nootropic;
KW   neuroprotective; cytostatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   144
FT                   /note= "N-glycosylated"
FT   Modified-site   174
FT                   /note= "O-glycosylated"
FT   Modified-site   216
FT                   /note= "O-glycosylated"
XX
PN   WO200260949-A2.
XX
PD   08-AUG-2002.
XX
PF   18-JAN-2002; 2002WO-US00510.
XX
PR   01-FEB-2001; 2001US-265749P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Jenkins N,  Witcher DR,  Wroblewski VJ;
XX
DR   WPI; 2002-599849/64.
XX
PT   FLINT isoforms which inhibit binding of Fas to FasL receptors, useful
PT   for treating or preventing a disease associated with diseases, such as
PT   inflammatory, autoimmune, infectious, cardiovascular and CNS disorders
PT   -
XX
```

```
PS   Disclosure; Page 37-38; 42pp; English.
XX
CC   The present sequence is the human Fas ligand inhibitory protein
CC   (FLINT) mature polypeptide.  FLINT is a glycoprotein involved in
CC   regulating apoptosis.  It binds Fas ligand (FasL), thereby
CC   preventing the interaction of FasL with Fas.  It also binds the
CC   ligand LIGHT to prevent its interaction with receptor LTBR, an
CC   otherwise initiating step in a second, independent apoptotic
CC   pathway.  The present invention provides FLINT isoforms having an
CC   average sialic acid content of 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5,
CC   4.0 or greater than 4.0 per molecule of FLINT.  These can be
CC   obtained by recombinant production, e.g. in AV12 RGT18 cells
CC   using recombinant plasmid pIG3-FLINT.  The FLINT isoforms are
CC   useful for treating or preventing a disease and/or condition that
CC   may be associated with the binding of Fas to FasL receptors, such
CC   as inflammatory/autoimmune diseases (rheumatoid arthritis,
CC   inflammatory bowel disease, graft-versus-host disease, diabetes,
CC   sepsis, pancreatitis, psoriasis, multiple sclerosis, Hashimoto's
CC   thyroiditis, Grave's disease, transplant rejection, systemic lupus
CC   erythematosus, autoimmune gastritis), infectious diseases
CC   (HIV-induced lymphopaenia, fulminant viral hepatitis, chronic
CC   hepatitis, cirrhosis), cardiovascular disorders (acute coronary
CC   syndrome, myocardial infarction, congestive heart failure,
CC   atherosclerosis, cerebral ischaemia, brain/spinal cord trauma) and
CC   central nervous system (CNS) disorders.  They may also be used as
CC   cytoprotection during cancer treatment, as an adjuvant to
CC   chemotherapy, prevention of acute lung injury and adult respiratory
CC   distress syndrome (ARDS).  The increased sialic acid content
CC   results in slower clearance time in vivo and enhanced therapeutic
CC   value.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 23;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 12
AAE14578
ID   AAE14578 standard; Protein; 271 AA.
XX
AC   AAE14578;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human mature FLINT protein.
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human.
XX
OS   Homo sapiens.
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
DR   N-PSDB; AAD27868.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page 29-30; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analog.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   mature FLINT protein.
XX
SQ   Sequence   271 AA;

  Query Match             100.0%;  Score 1491;  DB 23;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 13
AAW66102
ID   AAW66102 standard; Protein; 300 AA.
XX
AC   AAW66102;
XX
DT   02-DEC-1998  (first entry)
```

```
XX
DE   Amino acid sequence of tumour necrosis related receptor (TR4).
XX
KW   Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW   inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW   autoimmune disease; transplant rejection; stroke; cancer;
KW   Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   EP861850-A1.
XX
PD   02-SEP-1998.
XX
PF   20-JAN-1998;   98EP-0300382.
XX
PR   04-FEB-1997;   97US-0794796.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Emery J,  Tan KB,  Truneh A,  Young PR;
XX
DR   WPI; 1998-508248/44.
DR   N-PSDB; AAV07654.
XX
PT   New DNA encoding tumour necrosis related receptor - used to treat
PT   and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
PT   diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
PT   restenosis, AIDS, bone disorders and cancer
XX
PS   Claim 1; Fig 1; 21pp; English.
XX
CC   This is the amino acid sequence of the human tumour necrosis related
CC   receptor (TR4), used in the method of the invention.  The TR4 protein
CC   or its agonist can be used to treat a subject in need of enhanced
CC   TR4 polypeptide activity.  The antagonist is used to inhibit TR4
CC   polypeptide activity.  The active agents can be used for the
CC   treatment and prevention of diseases such as chronic and acute
CC   inflammation, arthritis, septicaemia, autoimmune diseases, transplant
CC   rejection, stroke, cancer, Alzheimer's disease.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1491;  DB 19;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 14
AAW63622
ID   AAW63622 standard; Protein; 300 AA.
XX
AC   AAW63622;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha protein.
XX
KW   Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW   endothelial cells; keratinocytes; normal prostate; apoptosis;
KW   prostate tumour tissue.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT   Protein         31..300
FT                   /note= "TNFR-6 alpha"
FT   Region          31..282
FT                   /note= "Soluble extracellular domain"
XX
PN   WO9830694-A2.
XX
PD   16-JUL-1998.
XX
PF   13-JAN-1998;   98WO-US00153.
XX
PR   14-JAN-1997;   97US-0035496.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ebner R,  Feng P,  Gentz RL,  Ni J,  Ruben SM,  Yu G;
XX
DR   WPI; 1998-399142/34.
DR   N-PSDB; AAV39085.
XX
PT   Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT   the diagnosis of immune system-related disorder(s)
XX
PS   Claim 20; Fig 1; 91pp; English.
XX
CC   The present sequence represents the human tumour necrosis factor
CC   receptor-6 alpha (TNFR-6 alpha) protein.  The invention also provides
CC   for the TNFR-6 beta protein (AAW63623).  TNFR-6 alpha and TNFR-6 beta
CC   are members of the tumour necrosis factor receptor (TNFR) family.  TNFRs
CC   are expressed in endothelial cells, keratinocytes, normal prostate and
CC   prostate tumour tissue.  For a number of disorders of these cells,
CC   particularly of the immune system, substantially altered (whether
CC   increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC   expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC   polypeptides, nucleic acids and antibodies are claimed to be useful in
CC   the diagnosis of such disorders.  Mutations of the TNFR-6 alpha and
CC   TNFR-6 beta genes can also be detected.  The TNFR polypeptides are
CC   also claimed to be useful for identifying ligands which may be useful
CC   in the treatment of apoptosis related disorders.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1491;  DB 19;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 15
AAY03099
ID   AAY03099 standard; Protein; 300 AA.
XX
AC   AAY03099;
XX
DT   09-DEC-1999  (first entry)
XX
DE   Human lung TNF-receptor protein.
XX
KW   Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
KW   detection; immunoassay; diagnosis; disease; immune system; tumour;
KW   osteogenic system; cardiovascular system; central nervous system; asthma;
KW   peripheral nervous systems; transplant incompatibility; antitumor;
KW   rheumatoid arthritis; antiasthmatic; antiarthritic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             134..1036
FT                   /*tag= a
FT                   /product= "TNF-receptor"
XX
PN   DE19809978-A1.
XX
PD   16-SEP-1999.
XX
PF   09-MAR-1998;   98DE-1009978.
XX
PR   09-MAR-1998;   98DE-1009978.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B; -
XX
DR   WPI; 1999-519473/44.
DR   N-PSDB; AAZ09998.
XX
PT   New soluble member of tumor necrosis factor receptor family, useful for
PT   identification specific modulators and for treating disease e.g. tumors
PT    -
XX
PS   Claim 1; Page 8-9; 10pp; German.
XX
CC   This invention describes a novel tumour necrosis factor (TNF) receptor
CC   (I) isolated from human lung tissue. (I) is used: (i) to raise specific
CC   antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
CC   (A), potential therapeutic agents; and (iii) therapeutically (optionally
CC   expressed from a gene therapy vector) in conditions associated with a
CC   deficit of (I). Ab are used: (a) for qualitative or quantitative
CC   detection of (I) in standard immunoassays (for diagnosis of disease, or
CC   susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
CC   cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
CC   used: (A) for recombinant production of (I); (B) also its oligonucleotide
CC   fragments, in standard hybridization and/or amplification assays; (C) as
CC   source of antisense molecules or ribozymes; and (D) to produce transgenic
CC   animals (for studying (patho)physiology of (I)). Diseases possibly
CC   associated with under- or over-expression of (I) are those of the immune,
CC   osteogenic, cardiovascular and central or peripheral nervous systems,
CC   tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
CC   products of the invention have antitumor, antiasthmatic and
CC   antiarthritic activity. This sequence represents the TNF-receptor of the
CC   invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1491;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-114;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


Search completed: December  3, 2003, 13:12:41
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                     GenCore version 5.1.6
              Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

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Perfect score:   1491
Sequence:        1 VAETPTYPWRDAETGERLVC..........RVARMPGLERSVRERFLPVH 271

Scoring table:   BLOSUM62
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Searched:        283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:       283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        PIR_76:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
                        %
Result                Query
  No.     Score       Match Length DB  ID                                   Description
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    1     340.5    22.8     461  1  A35356                                 tumor necrosis fac
    2     333.5    22.4     459  2  I48854                                 gene murine tumour
    3     332.5    22.3     474  2  B38634                                 tumor necrosis fac
    4     299.5    20.1     435  2  I54182                                 tumor necrosis fac
    5       289    19.4     651  2  JC7705                                 death receptor-6 -
    6       260    17.4     348  2  T28623                                 hypothetical prote
    7       260    17.4     349  2  D72175                                 G2R protein - vari
    8       260    17.4     349  2  D36858                                 gene G4R protein -
    9     234.5    15.7     325  2  B43692                                 T2 protein - rabbi
   10     215.5    14.5     277  2  I37552                                 OX40 homolog - hum
   11     211.5    14.2     271  2  S12783                                 OX40 antigen precu
   12       211    14.2     277  2  A60771                                 B-cell activation
   13     210.5    14.1     326  1  GQVZML                                 T2 protein - myxom
   14       203    13.6     305  2  A46476                                 B cell-associated
   15     194.5    13.0     272  2  I48700                                 gene ox40 protein
   16       185    12.4     256  2  B32393                                 T-cell antigen 4-1
   17       182    12.2     595  2  A42086                                 CD30 antigen precu
   18       174    11.7     255  2  I38426                                 lymphocyte activat
   19     171.5    11.5     416  1  JN0006                                 nerve growth facto
   20       168    11.3     425  1  A26431                                 nerve growth facto
   21       158    10.6     427  1  GQHUN                                  nerve growth facto
   22     155.5    10.4     327  2  A46484                                 apoptosis-mediatin
   23     148.5    10.0    1574  2  T13954                                 MEGF6 protein - ra
   24       148     9.9     250  1  A49053                                 CD27 antigen precu
   25     147.5     9.9    5376  2  T42215                                 zonadhesin - mouse
   26     146.5     9.8     260  1  A46517                                 CD27 antigen precu
   27       145     9.7     335  2  A40036                                 apoptosis-mediatin
   28       143     9.6    1620  2  T27283                                 hypothetical prote
   29       140     9.4     314  2  I37383                                 FAS soluble protei
```

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   30     137.5     9.2     324  2  JC2395                                 Fas antigen precur
   31     135.5     9.1    1299  2  T43251                                 furin (EC 3.4.21.7
   32       135     9.1    2321  2  S78549                                 notch3 protein - h
   33     130.5     8.8     454  1  GQMST1                                 tumor necrosis fac
   34     128.5     8.6    3635  2  T10053                                 laminin alpha 5 ch
   35       127     8.5    1192  2  S69000                                 laminin gamma 2 ch
   36     125.5     8.4    1548  2  S34583                                 serine proteinase
   37     124.5     8.4    1713  2  A55347                                 adhesive ligand ep
   38     123.5     8.3     455  1  GQHUT1                                 tumor necrosis fac
   39     123.5     8.3     493  2  JC5486                                 membrane glycoprot
   40     122.5     8.2    2824  2  T22759                                 hypothetical prote
   41       121     8.1    3106  1  S53868                                 laminin alpha-2 ch
   42       120     8.0    1609  1  MMHUB2                                 laminin gamma-1 ch
   43     119.5     8.0    3084  1  MMMSA                                  laminin alpha-1 ch
   44     118.5     7.9     461  1  GQRTT1                                 tumor necrosis fac
   45     118.5     7.9    1680  2  A43434                                 furin (EC 3.4.21.7

                                  ALIGNMENTS

RESULT 1
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
```

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R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             22.8%;  Score 340.5;  DB 1;  Length 461;
  Best Local Similarity   29.7%;  Pred. No. 2e-18;
  Matches   89;  Conservative   43;  Mismatches  115;  Indels   53;  Gaps   11;

Qy          1 VAETPTYPWRDAETGE------------RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRH 48
              || ||  |    | |             :: |::| ||   :  | : | | |  |
Db         27 VAFTPYAP----EPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82

Qy         49 YTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAG------FCLEHAS 102
              ||| ||::  |  |   |   : | :||    || | || |::           |
Db         83 YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK 142

Qy        103 CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT 162
              | || ||  ||| : :  |:|| ||||  ::||:: |:||: |  :     :||::| |
Db        143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA----IPGNASMDA 198

Qy        163 LCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE-----GWGPTP 217
              :||| :  |  :  |||    : |           :  |   :   ||        ||:|
Db        199 VCTSTS--PTRSMAPGAVHLPQPV-------STRSQHTQPTPEPSTAPSTSFLLPMGPSP 249

Qy        218 RA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL---RVARMP-GLERSVRERFLP 269
               |    |  || : |   :| |     | |:: ::  :   :| : |  |:|  :   ||
Db        250 PAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP 304

RESULT 2
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>

  Query Match             22.4%;  Score 333.5;  DB 2;  Length 459;
  Best Local Similarity   29.7%;  Pred. No. 6.8e-18;
  Matches   81;  Conservative   43;  Mismatches  110;  Indels   39;  Gaps    9;

Qy         17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
              :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   :  |||
Db         37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC 96

Qy         77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                  || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db         97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156

Qy        130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
              | ::||:: |:||| |: |     :||::| | :|     : :  |  :  |   |
Db        157 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 212

Qy        186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
               :|    |:    :   :| :|      | ||       |  :| : |   :| |
Db        213 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257

Qy        241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
              | |:: |:       |  :   |:|  :   :|
Db        258 GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 290

RESULT 3
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

  Query Match             22.3%;  Score 332.5;  DB 2;  Length 474;
  Best Local Similarity   29.7%;  Pred. No. 8.4e-18;
  Matches   81;  Conservative   44;  Mismatches  109;  Indels   39;  Gaps    9;
```

```
Qy          17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
               :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db          52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRAC 111

Qy          77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                   || | |  | :     |:|    |: :  | || ||  :   |: |  |: | ||||
Db         112 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 171

Qy         130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
               | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db         172 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227

Qy         186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
                :|    |:    :   :| :|      | ||       |  :| : |   :| |
Db         228 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

Qy         241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
               | |:: |:  :    |  :   |:|  :   :|
Db         273 GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP 305

RESULT 4
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

  Query Match             20.1%;  Score 299.5;  DB 2;  Length 435;
  Best Local Similarity   32.0%;  Pred. No. 2.4e-15;
  Matches   74;  Conservative   27;  Mismatches  101;  Indels   29;  Gaps    9;

Qy          13 ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
               |   |: |::|||||:|   | |   | |  |    | : ||||   : || |: : |
Db          52 EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109

Qy          70 EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
                ||   | :     |||: | |  | : ||  |    : ||||    :       |  |
Db         110 LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 168

Qy         123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC 182
               ||  | |  :|| | :||||  |   ||    ||::  || | :    ||   : |
Db         169 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLM 227

Qy         183 ERAVIDFVAFQDIS-------------IKRLQRLLQALEAPEGWGPTPRAG 220
                  ::    |  ::              ::|  ||:    |:| || | ||
Db         228 LAVLLPLAFFLLLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276

RESULT 5
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match             19.4%;  Score 289;  DB 2;  Length 651;
  Best Local Similarity   33.5%;  Pred. No. 2.2e-14;
  Matches   54;  Conservative   27;  Mismatches   80;  Indels    0;  Gaps    0;

Qy          11 DAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGERE 70
               |  | : |:| :|| ||:|  : | : :   | |||   :|:  | :||| |   |
Db          43 DRATNQELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPM 102

Qy          71 EEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
                |   | |  :| | | :| |     |: :  || | ||   || ::: :|:||  ||||
Db         103 IEKTHCTALTDRECTCLSGTFQINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162

Qy         131 ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFP 171
                  ||  :|: : :|    : :  ||:   | :| |    |
Db         163 DVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVCXSPASLP 203

RESULT 6
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

  Query Match             17.4%;  Score 260;  DB 2;  Length 348;
  Best Local Similarity   32.2%;  Pred. No. 1.9e-12;
  Matches   59;  Conservative   26;  Mismatches   90;  Indels    8;  Gaps    3;

Qy           5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
               |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db          27 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 86

Qy          64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                 |   : | |:|: |||| | |  |::      :    |:    |  | || :  |
Db          87 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 145

Qy         118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
               :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db         146 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 205

Qy         178 GAE 180
                :|
Db         206 TSE 208

RESULT 7
D72175
```

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G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Accession: D72175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

  Query Match             17.4%;  Score 260;  DB 2;  Length 349;
  Best Local Similarity   32.2%;  Pred. No. 1.9e-12;
  Matches   59;  Conservative   26;  Mismatches   90;  Indels    8;  Gaps    3;

Qy            5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
                |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db           28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87

Qy           64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                  |   : | |:|: |||| | |  |::      :    |:    |  | || :  |
Db           88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146

Qy          118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
                :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db          147 DVICSPCGFGTYSYTVSSTDKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 206

Qy          178 GAE 180
                 :|
Db          207 TSE 209


RESULT 8
D36858
gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NG>>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>

  Query Match             17.4%;  Score 260;  DB 2;  Length 349;
  Best Local Similarity   32.2%;  Pred. No. 1.9e-12;
  Matches   59;  Conservative   26;  Mismatches   90;  Indels    8;  Gaps    3;

Qy            5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
                |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db           28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87

Qy           64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                  |   : | |:|: |||| | |  |::      :    |:    |  | || :  |
Db           88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146

Qy          118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
                :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
Db          147 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 206

Qy          178 GAE 180
                 :|
Db          207 TSE 209


RESULT 9
B43692
T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A;Reference number: A43692; MUID:87321103; PMID:2820128
A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB:M17433
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>

  Query Match             15.7%;  Score 234.5;  DB 2;  Length 325;
  Best Local Similarity   32.9%;  Pred. No. 1.5e-10;
  Matches   52;  Conservative   19;  Mismatches   76;  Indels   11;  Gaps    3;

Qy           18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH 77
                | || | || :  | |   | | | ||    :|   |:   |  |   |     |:: |
Db           38 LCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLSESQPCD 97

Qy           78 ATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
                 ||:| | | || :           |     || | || :  | : :| |: ||| |:|
Db           98 RTHDRVCNCSTGNYCLLKGQNGCRICAPQTKCPAGYGV-SGHTRAGDTLCEKCPPHTYSD 156

Qy          132 SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTG 169
                | | :|:|    |  ::|  |       ::| ||:  |
Db          157 SLSPTERCGTSFNYISVGFNL----YPVNETSCTTTAG 190


RESULT 10
I37552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona
Eur. J. Immunol. 24, 677-683, 1994
```

```
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             14.5%;  Score 215.5;  DB 2;  Length 277;
  Best Local Similarity   27.0%;  Pred. No. 3.4e-09;
  Matches   72;  Conservative   22;  Mismatches  104;  Indels   69;  Gaps   11;

Qy          6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
              |||  |        | :| ||  :   | |   | | || |  |    :    : | :||
Db         35 TYPSNDR------CCHECRPGNGMVSRCSRSQNTVCRPCGPGFYNDVVSSKPCKPCTWCN 88

Qy         64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQP 123
              :  |   |  : | || :  |||| |            |  ||              | |
Db         89 LRSG--SERKQLCTATQDTVCRCRAG-------TQPLDSYKPG------------VDCAP 127

Qy        124 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTS---CTGFPLSTRVPGAE 180
              |||| |  |   :: |:|  |||  |     | |:| | :|         |  |: | |
Db        128 CPPGHF--SPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQPQETQGPPAR 185

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGW-----GPTPR-----AGRAALQLKLRR 230
                                        ::  | |     ||: |      |||   :
Db        186 PI-----------------------TVQPTEAWPRTSQGPSTRPVEVPGGRAVAAILGLG 222

Qy        231 RLTELLGAQDGALLVRLLQALRVARMP 257
               :  |||    |:|: |    |  |:|
Db        223 LVLGLLGPL--AILLALYLLRRDQRLP 247


RESULT 11
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>

  Query Match             14.2%;  Score 211.5;  DB 2;  Length 271;
  Best Local Similarity   31.5%;  Pred. No. 6.7e-09;
  Matches   53;  Conservative   18;  Mismatches   54;  Indels   43;  Gaps    8;

Qy          6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
              |||     :| :  | :| ||  :   |     | | || |  | :  ||   ::|  ||
Db         30 TYP-----SGHK-CCRECQPGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCN 83

Qy         64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
                 |   |  : |  | :  |:||                        ||| | |::
Db         84 HRSG--SELKQNCTPTEDTVCQCR------------------------PGTQPRQDSSHK 117

Qy        120 ---QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                  | ||||| |  |  |:: |:|  |||  |  :  | |:| ||:|
Db        118 LGVDCVPCPPGHF--SPGSNQACKPWTNCTLSGKQIRHPASNSLDTVC 163

RESULT 12
```

```
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             14.2%;  Score 211;  DB 2;  Length 277;
  Best Local Similarity   30.5%;  Pred. No. 7.5e-09;
  Matches   46;  Conservative   21;  Mismatches   76;  Indels    8;  Gaps    3;

Qy         20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
              |: | ||  :   |   : | | ||    :   ||    |   :||:   | | ::
Db         38 CSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTS 97

Qy         77 HATHNRACRCRTGFFAHA---GFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
                  :  | |  |:   :     |: | || || ||    |   :| |:||| | ||  |
Db         98 ET--DTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVS 155

Qy        134 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
              |: |:| |  :|    | :   |::  | :|
Db        156 SAFEKCHPWTSCETKDLVVQQAGINKTDVVC 186


RESULT 13
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             14.1%;  Score 210.5;  DB 1;  Length 326;
```

```
  Best Local Similarity   30.4%;  Pred. No. 9.6e-09;
  Matches   48;  Conservative   19;  Mismatches   80;  Indels   11;  Gaps    3;

Qy         18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH 77
              | |  ||||::  | |   | | | ||    :|   |:   |  |   |     |:::|
Db         38 LCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCD 97

Qy         78 ATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
               | :| | |  | :           |     || | || :  | : :  |  ||  |:|
Db         98 KTRDRVCDCSAGNYCLLKGQEGCRICAPKTKCPAGYGV-SGHTRTGDVLCTKCPRYTYSD 156

Qy        132 SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTG 169
              : ||:| |    |  ::   |       :|| ||:  |
Db        157 AVSSTETCTSSFNYISVEFNL----YPVNDTSCTTTAG 190


RESULT 14
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
A;Accession: A46476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <TOR>
A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

  Query Match             13.6%;  Score 203;  DB 2;  Length 305;
  Best Local Similarity   31.1%;  Pred. No. 3.3e-08;
  Matches   47;  Conservative   19;  Mismatches   77;  Indels    8;  Gaps    3;

Qy         20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
              |  | ||: :   |     | | ||    ::  ||   ||   |:|    | | ::
Db         38 CDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGT- 96

Qy         77 HATHNRACRCRTGFFA---HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 133
               |  :  | |: |          | :|  | || ||:   | : :| | ||| | ||  |
Db         97 -AESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQS 155

Qy        134 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
              |  |:| |  :|    | :   |:|  : :|
Db        156 SLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186


RESULT 15
I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell in
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             13.0%;  Score 194.5;  DB 2;  Length 272;
  Best Local Similarity   30.4%;  Pred. No. 1.3e-07;
  Matches   51;  Conservative   16;  Mismatches   58;  Indels   43;  Gaps    8;

Qy          6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNY--LERCRYCN 63
              |||     :| :  | :| ||  :   |     | | ||    | :  ||   ::|  ||
Db         31 TYP-----SGHK-CCRECQPGHGMVSRCDHTRDTLCHPCETGFYNEAVNYDTCKQCTQCN 84

Qy         64 VLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGT-PSQNT--- 119
                 |   |  : |  | :  ||||                        ||| | |::
Db         85 HRSG--SELKQNCTPTQDTVCRCR------------------------PGTQPRQDSGYK 118

Qy        120 ---QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLC 164
                  | |||||  |  |  ::: |:|  |||  |     | | | | :|
Db        119 LGVDCVPCPPGHF--SPGNNQACKPWTNCTLSGKQTRHPASDSLDAVC 164


Search completed: December  3, 2003, 13:14:38
Job time : 21 secs
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         December  3, 2003, 13:07:31 ; Search time 17 Seconds
                                              (without alignments)
                                              749.661 Million cell updates/sec

Title:          US-10-069-385-1
Perfect score:  1491
Sequence:       1 VAETPTYPWRDAETGERLVC..........RVARMPGLERSVRERFLPVH 271

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:      127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_41:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                     %
Result              Query
  No.     Score     Match Length DB  ID                        Description
-------------------------------------------------------------------------------
     1     1491     100.0    300  1  TR6B_HUMAN                O95407 homo sapien
     2    440.5      29.5    401  1  T11B_HUMAN                O00300 homo sapien
     3    425.5      28.5    401  1  T11B_RAT                  O08727 rattus norv
     4    424.5      28.5    401  1  T11B_MOUSE                O08712 mus musculu
     5    340.5      22.8    461  1  TR1B_HUMAN                P20333 homo sapien
     6    332.5      22.3    474  1  TR1B_MOUSE                P25119 mus musculu
     7    299.5      20.1    435  1  TNR3_HUMAN                P36941 homo sapien
     8    288.5      19.3    655  1  TR21_MOUSE                Q9epu5 mus musculu
     9      287      19.2    655  1  TR21_HUMAN                O75509 homo sapien
    10    265.5      17.8    415  1  TNR3_MOUSE                P50284 mus musculu
    11      260      17.4    349  1  CRMB_VARV                 P34015 variola vir
    12    257.5      17.3    349  1  CRMB_CAMPS                Q8uya7 camelpox vi
    13    254.5      17.1    351  1  CRMB_COWPX                O73559 cowpox viru
    14      244      16.4    283  1  TR14_HUMAN                Q92956 homo sapien
    15    235.5      15.8    616  1  TR11_HUMAN                Q9y6q6 homo sapien
    16    234.5      15.7    325  1  VT2_SFVKA                 P25943 shope fibro
    17    220.5      14.8    625  1  TR11_MOUSE                O35305 mus musculu
    18    215.5      14.5    277  1  TNR4_HUMAN                P43489 homo sapien
    19    211.5      14.2    271  1  TNR4_RAT                  P15725 rattus norv
    20      211      14.2    277  1  TNR5_HUMAN                P25942 homo sapien
    21    210.5      14.1    326  1  VT2_MYXVL                 P29825 myxoma viru
    22      203      13.6    289  1  TNR5_MOUSE                P27512 mus musculu
    23      202      13.5    269  1  TNR5_BOVIN                Q28203 bos taurus
    24    194.5      13.0    272  1  TNR4_MOUSE                P47741 mus musculu
    25      185      12.4    256  1  TNR9_MOUSE                P20334 mus musculu
    26      182      12.2    595  1  TNR8_HUMAN                P28908 homo sapien
    27      174      11.7    255  1  TNR9_HUMAN                Q07011 homo sapien
    28    171.5      11.5    416  1  TR16_CHICK                P18519 gallus gall
    29      171      11.5    180  1  TR22_MOUSE                Q9er62 mus musculu
    30      168      11.3    425  1  TR16_RAT                  P07174 rattus norv
    31      163      10.9    332  1  TNR6_PIG                  O77736 sus scrofa
    32      162      10.9    417  1  TR16_MOUSE                Q9z0w1 mus musculu
    33      158      10.6    427  1  TR16_HUMAN                P08138 homo sapien
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    34    155.5      10.4    327  1  TNR6_MOUSE                P25446 mus musculu
    35      155      10.4    323  1  TNR6_BOVIN                P51867 bos taurus
    36      153      10.3    241  1  TR18_HUMAN                Q9y5u5 homo sapien
    37    152.5      10.2    430  1  TRLT_MACFA                Q9n092 macaca fasc
    38    151.5      10.2    430  1  TRLT_HUMAN                Q969z4 homo sapien
    39    148.5      10.0    176  1  TR23_MOUSE                Q9er63 mus musculu
    40      148       9.9    250  1  TNR7_MOUSE                P41272 mus musculu
    41    147.5       9.9   5376  1  ZAN_MOUSE                 O88799 mus musculu
    42      145       9.7    335  1  TNR6_HUMAN                P25445 homo sapien
    43    143.5       9.6    471  1  TR1A_BOVIN                O19131 bos taurus
    44    142.5       9.6    260  1  TNR7_HUMAN                P26842 homo sapien
    45    137.5       9.2    324  1  TNR6_RAT                  Q63199 rattus norv

                                   ALIGNMENTS

RESULT 1
TR6B_HUMAN
ID   TR6B_HUMAN     STANDARD;      PRT;   300 AA.
AC   O95407;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE   receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68).
GN   TNFRSF6B OR DCR3 OR TR6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal lung;
RX   MEDLINE=99087326; PubMed=9872321;
RA   Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA   Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA   Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA   Goddard A.D., Botstein D., Ashkenazi A.;
RT   "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT   colon cancer.";
RL   Nature 396:699-703(1998).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC   TISSUE=Prostate;
RX   MEDLINE=99253915; PubMed=10318773;
RA   Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT   "A newly identified member of tumor necrosis factor receptor
RT   superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL   J. Biol. Chem. 274:13733-13736(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=20122600; PubMed=10655513;
RA   Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA   Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT   "Overexpression of M68/DcR3 in human gastrointestinal tract tumors
RT   independent of gene amplification and its location in a four-gene
RT   cluster.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Matthews L.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung, and Skin;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
CC       and TNFSF6/FasL. Protects against apoptosis.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
CC       Detected in adult stomach, spinal cord, lymph node, trachea,
CC       spleen, colon and lung. Highly expressed in several primary tumors
CC       from colon, stomach, rectum, esophagus and in SW480 colon
CC       carcinoma cells.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AF104419; AAD03056.1; -.
DR   EMBL; AF134240; AAD29688.1; -.
DR   EMBL; AF217796; AAF35244.1; -.
DR   EMBL; AF217793; AAF33685.1; -.
DR   EMBL; AF217794; AAF33686.1; -.
DR   EMBL; AL121845; CAC03668.1; -.
DR   EMBL; BC017065; AAH17065.1; -.
DR   EMBL; BC034349; AAH34349.1; -.
DR   HSSP; O14763; 1D0G.
DR   Genew; HGNC:11921; TNFRSF6B.
DR   MIM; 603361; -.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006916; P:anti-apoptosis; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    300       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 6B.
FT   REPEAT       31     70       TNFR-CYS 1.
FT   REPEAT       72    113       TNFR-CYS 2.
FT   REPEAT      115    150       TNFR-CYS 3.
FT   REPEAT      152    193       TNFR-CYS 4.
FT   DISULFID     49     62       BY SIMILARITY.
FT   DISULFID     52     70       BY SIMILARITY.
FT   DISULFID     73     88       BY SIMILARITY.
FT   DISULFID     91    105       BY SIMILARITY.
FT   DISULFID     95    113       BY SIMILARITY.
FT   DISULFID    115    126       BY SIMILARITY.
FT   DISULFID    132    150       BY SIMILARITY.
FT   DISULFID    153    168       BY SIMILARITY.
FT   DISULFID    174    193       BY SIMILARITY.
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32679 MW;  F9CAEE33718449AF CRC64;
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  Query Match             100.0%;  Score 1491;  DB 1;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-108;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89

Qy         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149

Qy        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Qy        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269

Qy        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
              |||||||||||||||||||||||||||||||
Db        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 2
T11B_HUMAN
ID   T11B_HUMAN     STANDARD;      PRT;   401 AA.
AC   O00300; O60236; Q9UHP4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung cancer;
RX   MEDLINE=98151033; PubMed=9492069;
RA   Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA   Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA   Tsuda E., Morinaga T., Higashio K.;
RT   "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT   osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT   osteoclastogenesis in vitro.";
RL   Endocrinology 139:1329-1337(1998).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Placenta;
RX   MEDLINE=98351569; PubMed=9688283;
RA   Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT   "Cloning and characterization of the gene encoding human
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL   Eur. J. Biochem. 254:685-691(1998).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
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RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 22-36 AND 378-401.
RX   MEDLINE=98238645; PubMed=9571159;
RA   Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA   Morinaga T., Tsuda E., Higashio K.;
RT   "Characterization of monomeric and homodimeric forms of
RT   osteoclastogenesis inhibitory factor.";
RL   Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN   [6]
RP   SEQUENCE OF 22-393 FROM N.A.
RC   TISSUE=Placenta;
RA   He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT   "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL   Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN   [7]
RP   SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX   MEDLINE=97312536; PubMed=9168977;
RA   Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA   Morinaga T., Higashio K.;
RT   "Isolation of a novel cytokine from human fibroblasts that
RT   specifically inhibits osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN   [8]
RP   TRAIL BINDING.
RX   MEDLINE=98269100; PubMed=9603945;
RA   Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA   Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA   James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT   "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL   J. Biol. Chem. 273:14363-14367(1998).
RN   [9]
RP   CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX   MEDLINE=98148058; PubMed=9478964;
RA   Yamaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
RA   Morinaga T., Higashio K.;
RT   "Characterization of structural domains of human osteoclastogenesis
RT   inhibitory factor.";
RL   J. Biol. Chem. 273:5117-5123(1998).
RN   [10]
RP   REVIEW.
RX   MEDLINE=21395914; PubMed=11505383;
RA   Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT   "Receptor activator of nuclear factor-kappaB ligand and
RT   osteoprotegerin: potential implications for the pathogenesis and
RT   treatment of malignant bone diseases.";
RL   Cancer 92:460-470(2001).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC       homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC       play a role in preventing arterial calcification. May act as decoy
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CC       receptor for TRAIL and protect against apoptosis. TRAIL binding
CC       blocks the inhibition of osteoclastogenesis.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC       liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC       lymph node, trachea, adrenal gland, testis, and bone marrow.
CC       Detected at very low levels in brain, placenta and skeletal
CC       muscle. Highly expressed in fetal kidney, liver and lung.
CC   -!- INDUCTION: Upregulated by increasing calcium-concentration in the
CC       medium and estrogens. Downregulated by glucocorticoids.
CC   -!- PTM: N-glycosylated. Contains sialic acid residues.
CC   -!- PTM: N-terminus may be blocked.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 2 death domains.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; U94332; AAB53709.1; -.
DR   EMBL; AB002146; BAA25910.1; -.
DR   EMBL; AB008822; BAA32076.1; -.
DR   EMBL; AB008821; BAA32076.1; JOINED.
DR   EMBL; BC030155; AAH30155.1; -.
DR   EMBL; AF134187; AAF20168.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:11909; TNFRSF11B.
DR   MIM; 602643; -.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0005125; F:cytokine activity; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0001501; P:skeletal development; TAS.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT   SIGNAL        1     21
FT   CHAIN        22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11B.
FT   REPEAT       24     62       TNFR-CYS 1.
FT   REPEAT       65    105       TNFR-CYS 2.
FT   REPEAT      107    142       TNFR-CYS 3.
FT   REPEAT      145    185       TNFR-CYS 4.
FT   DOMAIN      198    269       DEATH 1.
FT   DOMAIN      270    365       DEATH 2.
FT   SITE        400    400       INVOLVED IN DIMERIZATION.
FT   DISULFID     41     54       BY SIMILARITY.
FT   DISULFID     44     62       BY SIMILARITY.
FT   DISULFID     65     80       BY SIMILARITY.
FT   DISULFID     83     97       BY SIMILARITY.
FT   DISULFID     87    105       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   DISULFID    124    142       BY SIMILARITY.
FT   DISULFID    145    160       BY SIMILARITY.
FT   DISULFID    166    185       BY SIMILARITY.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT       3      3       K -> N.
FT                                /FTId=VAR_013439.
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FT   MUTAGEN     400    400       C->S: ABOLISHES DIMERIZATION.
FT   MUTAGEN     400    401       MISSING: ABOLISHES DIMERIZATION.
FT   CONFLICT    263    263       D -> A (IN REF. 1).
SQ   SEQUENCE   401 AA;  46040 MW;  EDF448B67D86C71E CRC64;

  Query Match             29.5%;  Score 440.5;  DB 1;  Length 401;
  Best Local Similarity   41.2%;  Pred. No. 4e-27;
  Matches   77;  Conservative   31;  Mismatches   74;  Indels    5;  Gaps    2;

Qy           5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
               | |   | ||  :|:| :|||||:::: |     | | |||  :||  |:  : | ||:
Db          26 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP 85

Qy          65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
               :| | :   : |: |||| | |: | :    |||:| ||||| ||:  ||| :|| |: |
Db          86 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 145

Qy         125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
               | | ||  :||   |: | ||:  || |   |:::|| :   |:|   ||:  | :   |
Db         146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202

Qy         183 ERAVIDF 189
               | |   |
Db         203 EEAFFRF 209


RESULT 3
T11B_RAT
ID   T11B_RAT       STANDARD;      PRT;   401 AA.
AC   O08727;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin).
GN   TNFRSF11B OR OPG.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic intestine;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC       seems to depend on the local RANKL/OPG ratio. May also play a role
CC       in preventing arterial calcification. May act as decoy receptor
CC       for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC       inhibition of osteoclastogenesis (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- INDUCTION: Upregulated by osteopontin.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 2 death domains.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U94330; AAB53707.1; -.
DR   HSSP; P25942; 1CDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11B.
FT   REPEAT       24     62       TNFR-CYS 1.
FT   REPEAT       65    105       TNFR-CYS 2.
FT   REPEAT      107    142       TNFR-CYS 3.
FT   REPEAT      145    185       TNFR-CYS 4.
FT   DOMAIN      198    269       DEATH 1.
FT   DOMAIN      270    365       DEATH 2.
FT   SITE        400    400       INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT   DISULFID     41     54       BY SIMILARITY.
FT   DISULFID     44     62       BY SIMILARITY.
FT   DISULFID     65     80       BY SIMILARITY.
FT   DISULFID     83     97       BY SIMILARITY.
FT   DISULFID     87    105       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   DISULFID    124    142       BY SIMILARITY.
FT   DISULFID    145    160       BY SIMILARITY.
FT   DISULFID    166    185       BY SIMILARITY.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   401 AA;  46192 MW;  FEC6A31F1D4E573A CRC64;

  Query Match             28.5%;  Score 425.5;  DB 1;  Length 401;
  Best Local Similarity   39.5%;  Pred. No. 5.8e-26;
  Matches   81;  Conservative   33;  Mismatches   86;  Indels    5;  Gaps    2;

Qy           5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
               | |   | ||| :|:| :| |||:::: |     | | |||   ||  |:  : | ||:
Db          26 PKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

Qy          65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
               :| | :   : |: |||| | |  | :    |||:| ||||| ||:  ||| :|| |: |
Db          86 VCKELQTVKQECNRTHNRVCECEEGRYLELEFCLKHRSCPPGLGVLQAGTPERNTVCKRC 145

Qy         125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
               | | ||  :||   |: | ||::||| |   |:::|| :   |:|   :|:  | :   |
Db         146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC 202

Qy         183 ERAVIDFVAFQDISIKRLQRLLQAL 207
               | |   |     |    |  |: :|
Db         203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 4
T11B_MOUSE
ID   T11B_MOUSE     STANDARD;      PRT;   401 AA.
AC   O08712; O70202;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
RP   AND ARG-296.
RC   STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX   MEDLINE=98382527; PubMed=9714833;
RA   Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA   Higashio K.;
RT   "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT   gene and its expression in embryogenesis.";
RL   Gene 215:339-343(1998).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=21060987; PubMed=10952716;
RA   Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA   Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA   Simonet W.S.;
RT   "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT   osteoclasts and prevents vascular calcification by blocking a process
RT   resembling osteoclastogenesis.";
RL   J. Exp. Med. 192:463-474(2000).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC       homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC       play a role in preventing arterial calcification. May act as decoy
CC       receptor for TRAIL and protect against apoptosis. TRAIL binding
CC       blocks the inhibition of osteoclastogenesis.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC       intestines and calvaria. Highly expressed in decidua and placenta,
CC       and in embryo.
CC   -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
CC       whereas expression decreases at day 11 and increases from day 15
CC       to 17. On day 15 found in developing bone primordia,
CC       brachiocephalic artery and ductus arteriosus, left main bronchus,
CC       abdominal aorta and midgut.
CC   -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
CC       1,25-dihdroxyvitamin D3 and parathyroid hormone.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 2 death domains.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U94331; AAB53708.1; -.
DR   EMBL; AB013898; BAA28269.1; -.
DR   EMBL; AB013903; BAA33388.1; -.
DR   EMBL; AB013899; BAA33388.1; JOINED.
DR   EMBL; AB013900; BAA33388.1; JOINED.
DR   EMBL; AB013901; BAA33388.1; JOINED.
DR   EMBL; AB013902; BAA33388.1; JOINED.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:109587; Tnfrsf11b.
DR   GO; GO:0005578; C:extracellular matrix; IDA.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11B.
FT   REPEAT       24     62       TNFR-CYS 1.
FT   REPEAT       65    105       TNFR-CYS 2.
FT   REPEAT      107    142       TNFR-CYS 3.
FT   REPEAT      145    185       TNFR-CYS 4.
FT   DOMAIN      198    269       DEATH 1.
FT   DOMAIN      283    365       DEATH 2.
FT   SITE        400    400       INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT   DISULFID     41     54       BY SIMILARITY.
FT   DISULFID     44     62       BY SIMILARITY.
FT   DISULFID     65     80       BY SIMILARITY.
FT   DISULFID     83     97       BY SIMILARITY.
FT   DISULFID     87    105       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   DISULFID    124    142       BY SIMILARITY.
FT   DISULFID    145    160       BY SIMILARITY.
FT   DISULFID    166    185       BY SIMILARITY.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     138    138       R -> P (IN STRAINS 129/OLA AND NIH
FT                                SWISS).
FT   VARIANT     161    161       I -> R (IN STRAINS 129/OLA AND NIH
FT                                SWISS).
FT   VARIANT     165    165       N -> D (IN STRAINS 129/OLA AND NIH
FT                                SWISS).
FT   VARIANT     288    288       S -> A (IN STRAINS 129/OLA AND NIH
FT                                SWISS).
FT   VARIANT     296    296       L -> R (IN STRAINS 129/OLA AND NIH
FT                                SWISS).
SQ   SEQUENCE   401 AA;  45923 MW;  CAA6102D3B312470 CRC64;

  Query Match             28.5%;  Score 424.5;  DB 1;  Length 401;
  Best Local Similarity   39.0%;  Pred. No. 7e-26;
  Matches   80;  Conservative   32;  Mismatches   88;  Indels    5;  Gaps    2;

Qy          5 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 64
              | |   | ||| :|:| :| |||:::: |     | | |||   ||  |:  : | ||:
Db         26 PKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSP 85

Qy         65 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 124
              :| | :   : |: |||| | |  | :    |||:| |||||:||:  ||| :|| |: |
Db         86 VCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKC 145

Qy        125 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 182
              | | ||  :||   |  | ||:  || |   |:::|| :   |:|   :|:  | :   |
Db        146 PDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNV---CSGNREATQKCGIDVTLC 202

Qy        183 ERAVIDFVAFQDISIKRLQRLLQAL 207
              | |   |     |    |  |: :|
Db        203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 5
TR1B_HUMAN
ID   TR1B_HUMAN     STANDARD;      PRT;   461 AA.
AC   P20333; Q16042; Q9UIH1;
DT   01-FEB-1991 (Rel. 17, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
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DE   [Contains: Tumor necrosis factor binding protein 2 (TBPII)].
GN   TNFRSF1B OR TNFR2 OR TNFBR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90260639; PubMed=2160731;
RA   Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA   Dower S.K., Cosman D., Goodwin R.G.;
RT   "A receptor for tumor necrosis factor defines an unusual family of
RT   cellular and viral proteins.";
RL   Science 248:1019-1023(1990).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANT ARG-196.
RX   MEDLINE=91045991; PubMed=2172983;
RA   Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA   Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT   "A second tumor necrosis factor receptor gene product can shed a
RT   naturally occurring tumor necrosis factor inhibitor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96299745; PubMed=8661109;
RA   Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA   Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA   Brodeur G.M.;
RT   "Physical mapping and genomic structure of the human TNFR2 gene.";
RL   Genomics 35:94-100(1996).
RN   [4]
RP   SEQUENCE OF 37-461 FROM N.A.
RX   MEDLINE=91370690; PubMed=1966549;
RA   Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA   Brockhaus M., Lesslauer W.;
RT   "Two human TNF receptors have similar extracellular, but distinct
RT   intracellular, domain sequences.";
RL   Cytokine 2:231-237(1990).
RN   [5]
RP   SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX   MEDLINE=90349572; PubMed=2166946;
RA   Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA   Ringold G.M.;
RT   "Complementary DNA cloning of a receptor for tumor necrosis factor
RT   and demonstration of a shed form of the receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN   [6]
RP   SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX   MEDLINE=21069356; PubMed=11197692;
RA   Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT   "New single nucleotide polymorphisms in the coding region of human
RT   TNFR2: association with systemic lupus erythematosus.";
RL   Genes Immun. 1:501-503(2000).
RN   [7]
RP   SEQUENCE OF 27-31.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [8]
RP   SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX   MEDLINE=91056048; PubMed=2173696;
RA   Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA   Brockhaus M.;
RT   "Purification and partial amino acid sequence analysis of two
RT   distinct tumor necrosis factor receptors from HL60 cells.";
RL   J. Biol. Chem. 265:20131-20138(1990).
RN   [9]
RP   CHARACTERIZATION.
RX   MEDLINE=93016040; PubMed=1328224;
RA   Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA   Lipari M.T., Goeddel D.V.;
RT   "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT   Characterization of ligand binding, internalization, and receptor
RT   phosphorylation.";
RL   J. Biol. Chem. 267:21172-21178(1992).
RN   [10]
RP   INTERACTION WITH TRAF2.
RX   MEDLINE=94349371; PubMed=8069916;
RA   Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT   "A novel family of putative signal transducers associated with the
RT   cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL   Cell 78:681-692(1994).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP   TRAF2.
RX   MEDLINE=99221490; PubMed=10206649;
RA   Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT   "Structural basis for self-association and receptor recognition of
RT   human TRAF2.";
RL   Nature 398:533-538(1999).
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC       apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
CC   -!- SUBUNIT: Binds to TRAF2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- PTM: Phosphorylated; mainly on serine residues and with a very low
CC       level on threonine residues.
CC   -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC       produced from the membrane form by proteolytic processing.
CC   -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC       Wyeth-Ayerst). Used to treat moderate to servere rheumatoid
CC       arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC       portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to
CC       TNF-alpha and blocks its interactions with receptors.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC   -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC       WWW="http://www.enbrel.com/".
CC
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   modified and this statement is not removed.  Usage  by  and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M32315; AAA59929.1; -.
DR   EMBL; U52165; AAC50622.1; -.
DR   EMBL; U52156; AAC50622.1; JOINED.
DR   EMBL; U52157; AAC50622.1; JOINED.
DR   EMBL; U52158; AAC50622.1; JOINED.
DR   EMBL; U52159; AAC50622.1; JOINED.
DR   EMBL; U52160; AAC50622.1; JOINED.
DR   EMBL; U52161; AAC50622.1; JOINED.
DR   EMBL; U52162; AAC50622.1; JOINED.
DR   EMBL; U52163; AAC50622.1; JOINED.
DR   EMBL; U52164; AAC50622.1; JOINED.
DR   EMBL; M55994; AAA36755.1; -.
DR   EMBL; S63368; AAB19824.2; -.
DR   EMBL; M35857; AAA63262.1; -.
DR   EMBL; AB030950; BAA89053.1; -.
DR   PIR; A35356; A35356.
DR   PDB; 1CA9; 12-APR-99.
DR   Genew; HGNC:11917; TNFRSF1B.
DR   MIM; 191191; -.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
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```
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Phosphorylation; Pharmaceutical; Polymorphism; 3D-structure.
FT   SIGNAL        1     22
FT   CHAIN        23    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 1B, MEMBRANE FORM.
FT   CHAIN        27      ?       TUMOR NECROSIS FACTOR BINDING PROTEIN 2.
FT   DOMAIN       23    257       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    258    287       POTENTIAL.
FT   DOMAIN      288    461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       39     76       TNFR-CYS 1.
FT   REPEAT       77    118       TNFR-CYS 2.
FT   REPEAT      119    162       TNFR-CYS 3.
FT   REPEAT      163    201       TNFR-CYS 4.
FT   DISULFID     40     53       BY SIMILARITY.
FT   DISULFID     54     67       BY SIMILARITY.
FT   DISULFID     57     75       BY SIMILARITY.
FT   DISULFID     78     93       BY SIMILARITY.
FT   DISULFID     96    110       BY SIMILARITY.
FT   DISULFID    100    118       BY SIMILARITY.
FT   DISULFID    120    126       BY SIMILARITY.
FT   DISULFID    134    143       BY SIMILARITY.
FT   DISULFID    137    161       BY SIMILARITY.
FT   DISULFID    164    179       BY SIMILARITY.
FT   CARBOHYD    171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    193    193       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     196    196       M -> R.
FT                                /FTId=VAR_015434.
FT   VARIANT     232    232       E -> K.
FT                                /FTId=VAR_015435.
FT   CONFLICT    141    141       R -> P (IN REF. 5).
FT   CONFLICT    363    363       A -> T (IN REF. 5).
SQ   SEQUENCE   461 AA;  48291 MW;  603D0AE1CD69ACBF CRC64;

  Query Match             22.8%;  Score 340.5;  DB 1;  Length 461;
  Best Local Similarity   29.7%;  Pred. No. 2.5e-19;
  Matches   89;  Conservative   43;  Mismatches  115;  Indels   53;  Gaps   11;

Qy          1 VAETPTYPWRDAETGE------------RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRH 48
              || ||  |    | |             :: |::| ||   :  | : | | |  |
Db         27 VAFTPYAP----EPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82

Qy         49 YTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAG------FCLEHAS 102
              ||| ||::  |  |   |   : | :||    || | || |::           |
Db         83 YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK 142

Qy        103 CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT 162
              | || ||  ||| : :  |:|| ||||| ::||:: |:||: |  :     :||::| |
Db        143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVA----IPGNASMDA 198

Qy        163 LCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE-----GWGPTP 217
              :||| :  |  :  |||    : |           :  |   :   ||        ||:|
Db        199 VCTSTS--PTRSMAPGAVHLPQPV-------STRSQHTQPTPEPSTAPSTSFLLPMGPSP 249

Qy        218 RA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL---RVARMP-GLERSVRERFLP 269
               |    |  || : :   :| |     | |:: ::  :   :| : |  |:|  :   ||
Db        250 PAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP 304


RESULT 6
TR1B_MOUSE
ID   TR1B_MOUSE     STANDARD;      PRT;   474 AA.
AC   P25119; P97893;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (TNF-R2) (p75).
GN   TNFRSF1B OR TNFR2 OR TNFR-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE OF 1-26 FROM N.A.
RC   STRAIN=NOD;
RA   Jacob C.O., Liu J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RA   Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC       apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By
CC       similarity).
CC   -!- SUBUNIT: Binds to TRAF2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M60469; AAA39752.1; -.
DR   EMBL; M59378; AAA40463.1; -.
DR   EMBL; U39488; AAA85021.1; -.
DR   EMBL; X87128; CAA60618.1; -.
DR   PIR; B38634; B38634.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
DR   GO; GO:0006954; P:inflammatory response; IMP.
DR   GO; GO:0008220; P:necrosis; IMP.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    474       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 1B.
FT   DOMAIN       23    258       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    259    288       POTENTIAL.
FT   DOMAIN      289    474       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       39     77       TNFR-CYS 1.
FT   REPEAT       78    119       TNFR-CYS 2.
FT   REPEAT      120    164       TNFR-CYS 3.
FT   REPEAT      165    203       TNFR-CYS 4.
FT   DISULFID     40     54       BY SIMILARITY.
FT   DISULFID     55     68       BY SIMILARITY.
FT   DISULFID     58     76       BY SIMILARITY.
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FT   DISULFID     79     94       BY SIMILARITY.
FT   DISULFID     97    111       BY SIMILARITY.
FT   DISULFID    101    119       BY SIMILARITY.
FT   DISULFID    121    127       BY SIMILARITY.
FT   DISULFID    136    145       BY SIMILARITY.
FT   DISULFID    139    163       BY SIMILARITY.
FT   DISULFID    166    181       BY SIMILARITY.
FT   CARBOHYD     69     69       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   474 AA;  50319 MW;  462EAE398C4D6563 CRC64;

  Query Match             22.3%;  Score 332.5;  DB 1;  Length 474;
  Best Local Similarity   29.7%;  Pred. No. 1.1e-18;
  Matches   81;  Conservative   44;  Mismatches  109;  Indels   39;  Gaps    9;

Qy         17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
              :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db         52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRAC 111

Qy         77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                  || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db        112 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 171

Qy        130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
              | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db        172 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227

Qy        186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
               :|    |:    :   :| :|      | ||       |  :| : |   :| |
Db        228 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

Qy        241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
              | |:: |:  :    |  :   |:|  :   :|
Db        273 GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP 305


RESULT 7
TNR3_HUMAN
ID   TNR3_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE   protein) (Tumor necrosis factor C receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=99223511; PubMed=10207006;
RA   Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT   "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT   death in HeLa cells.";
RL   J. Biol. Chem. 274:11868-11873(1999).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=20261554; PubMed=10799510;
RA   Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA   Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT   "The lymphotoxin-beta receptor is necessary and sufficient for
RT   LIGHT-mediated apoptosis of tumor cells.";
RL   J. Biol. Chem. 275:14307-14315(2000).
RN   [6]
RP   INTERACTION WITH TRAF3.
RX   MEDLINE=96278943; PubMed=8663299;
RA   Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA   Yagita H., Okumura K.;
RT   "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT   the lymphotoxin-beta receptor.";
RL   J. Biol. Chem. 271:14661-14664(1996).
RN   [7]
RP   INTERACTION WITH TRAF4.
RX   PubMed=9626059;
RA   Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
RA   Gascoyne R.D., Berern K., McFadden D., Shabaik A., Hugh J.,
RA   Reynolds A., Clevenger C.V., Reed J.C.;
RT   "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT   adult, fetal, and tumor tissues.";
RL   Am. J. Pathol. 152:1549-1561(1998).
RN   [8]
RP   INTERACTION WITH TRAF5.
RX   MEDLINE=98172745; PubMed=9511754;
RA   Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA   Otsuka M., Yamamoto T., Inoue J.-I.;
RT   "Cloning and characterization of a cDNA encoding the human homolog of
RT   tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL   Gene 207:135-140(1998).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs.
CC   -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
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DR   EMBL; BC026262; AAH26262.1; -.
DR   PIR; I54182; I54182.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:6718; LTBR.
DR   MIM; 600979; -.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    435       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 3.
FT   DOMAIN       31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    228    248       POTENTIAL.
FT   DOMAIN      249    435       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    168       TNFR-CYS 3.
FT   REPEAT      169    211       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    148       BY SIMILARITY.
FT   DISULFID    142    167       BY SIMILARITY.
FT   DISULFID    170    185       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;

  Query Match             20.1%;  Score 299.5;  DB 1;  Length 435;
  Best Local Similarity   32.0%;  Pred. No. 3.5e-16;
  Matches   74;  Conservative   27;  Mismatches  101;  Indels   29;  Gaps    9;

Qy         13 ETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGER 69
              |   |: |::|||||:|   | |   | |  |    | : ||||   : || |: : |
Db         52 EPQHRICCSRCPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG-- 109

Qy         70 EEEARACHATHNRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQ 122
               ||   | :     |||: | |  | : ||  |    : ||||    :       |  |
Db        110 LEEIAPCTSKRKTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCV 168

Qy        123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEEC 182
              ||  | |  :|| | :||||  |   ||    ||::  || | :    ||   : |
Db        169 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLM 227

Qy        183 ERAVIDFVAFQDIS-------------IKRLQRLLQALEAPEGWGPTPRAG 220
                 ::    |  ::              ::|  ||:    |:| || | ||
Db        228 LAVLLPLAFFLLLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276


RESULT 8
TR21_MOUSE
ID   TR21_MOUSE     STANDARD;      PRT;   655 AA.
AC   Q9EPU5; Q91W77; Q91XH9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE   related death receptor-6) (Death receptor 6).
GN   TNFRSF21 OR DR6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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RC   STRAIN=C57BL/6; TISSUE=Kidney;
RA   Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA   Minami M.;
RT   "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT   (DR6).";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Kidney;
RA   Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT   "Murine DR6: murine TNFR-related death receptor-6.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=21571606; PubMed=11714751;
RA   Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT   "Impaired c-Jun amino terminal kinase activity and T cell
RT   differentiation in death receptor 6-deficient mice.";
RL   J. Exp. Med. 194:1441-1448(2001).
CC   -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC       similarity). May activate JNK and be involved in T-cell
CC       differentiation.
CC   -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC       May be involved in T-cell differentiation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC       thymus, testis, prostate, ovary, small intestine, colon, brain,
CC       lung and kidney, and in fetal brain, liver and lung. Detected at
CC       lower levels in adult peripheral blood leukocytes, lung, and in
CC       fetal muscle, heart, kidney, small intestine and skin. Detected in
CC       T-cells, B-cells and monocytes. In T-cells expression is highest
CC       in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF322069; AAG38115.1; -.
DR   EMBL; AY043489; AAK74193.1; -.
DR   EMBL; BC016420; AAH16420.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:2151075; Tnfrsf21.
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DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     41       POTENTIAL.
FT   CHAIN        42    655       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 21.
FT   DOMAIN       42    349       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    350    370       POTENTIAL.
FT   DOMAIN      371    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      415    498       DEATH.
FT   REPEAT       50     88       TNFR-CYS 1.
FT   REPEAT       90    131       TNFR-CYS 2.
FT   REPEAT      133    167       TNFR-CYS 3.
FT   REPEAT      170    211       TNFR-CYS 4.
FT   DISULFID     67     80       BY SIMILARITY.
FT   DISULFID     70     88       BY SIMILARITY.
FT   DISULFID     91    106       BY SIMILARITY.
FT   DISULFID    109    123       BY SIMILARITY.
FT   DISULFID    113    131       BY SIMILARITY.
FT   DISULFID    133    144       BY SIMILARITY.
FT   DISULFID    150    168       BY SIMILARITY.
FT   DISULFID    171    186       BY SIMILARITY.
FT   DISULFID    192    211       BY SIMILARITY.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    252    252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    257    257       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    352    352       W -> L (IN REF. 1).
FT   CONFLICT    523    523       M -> I (IN REF. 3).
SQ   SEQUENCE   655 AA;  71982 MW;  5EC7C51C7C99EFF7 CRC64;

  Query Match             19.3%;  Score 288.5;  DB 1;  Length 655;
  Best Local Similarity   29.7%;  Pred. No. 3.8e-15;
  Matches   69;  Conservative   32;  Mismatches  116;  Indels   15;  Gaps    3;

Qy          6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
              ||   |  ||: | | :|| ||:|   |   |   |  ||   :|:  | :|||  |:  
Db         53 TYRHVDRTTGQVLTCDKCPAGTYVSEHCTNMSLRVCSSCPAGTFTRHENGIERCHDCSQP 112

Qy         66 CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCP 125
              |     |   | |  :| | |  | :     |  |  || | ||   || ::: :|: | 
Db        113 CPWPMIERLPCAALTDRECICPPGMYQSNGTCAPHTVCPVGWGVRKKGTENEDVRCKQCA 172

Qy        126 PGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPL---STRVPGAEEC 182
               ||||   ||  :|: | :|    | :  ||:   | :|    |  |   ||  | :   
Db        173 RGTFSDVPSSVMKCKAHTDCLGQNLEVVKPGTKETDNVC----GMRLFFSSTNPPSSGTV 228

Qy        183 ERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTE 234
                :  : :   |:     :        |:|   |     |::: |:   : |
Db        229 TFSHPEHMESHDVPSSTYE--------PQGMNSTDSNSTASVRTKVPSGIEE 272


RESULT 9
TR21_HUMAN
ID   TR21_HUMAN     STANDARD;      PRT;   655 AA.
AC   O75509; Q96D86;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE   related death receptor-6) (Death receptor 6).
GN   TNFRSF21 OR DR6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98378343; PubMed=9714541;
RA   Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C.,
RA   Aggarwal B.B., Ni J., Dixit V.M.;
RT   "Identification and functional characterization of DR6, a novel death
RT   domain-containing TNF receptor.";
RL   FEBS Lett. 431:351-356(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Parker A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC   -!- SUBUNIT: Associates with TRADD.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
CC       pancreas, lymph node, thymus and prostate. Detected at lower
CC       levels in lung, skeletal muscle, kidney, testis, uterus, small
CC       intestine, colon, spleen, bone marrow and fetal liver. Very low
CC       levels were found in adult liver and peripheral blood leukocytes.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF068868; AAC34583.1; -.
DR   EMBL; AL096801; -; NOT_ANNOTATED_CDS.
DR   EMBL; BC017730; AAH17730.1; -.
DR   EMBL; BC010241; AAH10241.1; ALT_INIT.
DR   HSSP; O14763; 1D0G.
DR   Genew; HGNC:13469; TNFRSF21.
DR   MIM; 605732; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
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DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     41       POTENTIAL.
FT   CHAIN        42    655       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 21.
FT   DOMAIN       42    349       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    350    370       POTENTIAL.
FT   DOMAIN      371    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      415    498       DEATH.
FT   REPEAT       50     88       TNFR-CYS 1.
FT   REPEAT       90    131       TNFR-CYS 2.
FT   REPEAT      133    167       TNFR-CYS 3.
FT   REPEAT      170    211       TNFR-CYS 4.
FT   DISULFID     67     80       BY SIMILARITY.
FT   DISULFID     70     88       BY SIMILARITY.
FT   DISULFID     91    106       BY SIMILARITY.
FT   DISULFID    109    123       BY SIMILARITY.
FT   DISULFID    113    131       BY SIMILARITY.
FT   DISULFID    133    144       BY SIMILARITY.
FT   DISULFID    150    168       BY SIMILARITY.
FT   DISULFID    171    186       BY SIMILARITY.
FT   DISULFID    192    211       BY SIMILARITY.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    252    252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    257    257       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   655 AA;  71844 MW;  48939391C4852A33 CRC64;

  Query Match             19.2%;  Score 287;  DB 1;  Length 655;
  Best Local Similarity   34.3%;  Pred. No. 5e-15;
  Matches   58;  Conservative   23;  Mismatches   88;  Indels    0;  Gaps    0;

Qy          6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
              ||   |  ||: | | :|| ||:|   |   |   |  ||   :|:  | :|:|  |:
Db         53 TYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQP 112

Qy         66 CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCP 125
              |     |   | |  :| | |  | |     |  |  || | ||   || ::: :|: |
Db        113 CPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCA 172

Qy        126 PGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLST 174
               ||||   ||  :|: : :| :  | :  ||:   | :| :   |  ||
Db        173 RGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSST 221


RESULT 10
TNR3_MOUSE
ID   TNR3_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
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RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
RN   [3]
RP   INTERACTION WITH TRAF5.
RC   STRAIN=BALB/c;
RX   MEDLINE=96278943; PubMed=8663299;
RA   Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
RA   Yagita H., Okumura K.;
RT   "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT   the lymphotoxin-beta receptor.";
RL   J. Biol. Chem. 271:14661-14664(1996).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs
CC       (By similarity).
CC   -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
CC       Associates with TRAF3 and TRAF4 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    415       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 3.
FT   DOMAIN       31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      245    415       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    170       TNFR-CYS 3.
FT   REPEAT      171    213       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    150       BY SIMILARITY.
FT   DISULFID    142    169       BY SIMILARITY.
FT   DISULFID    172    187       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AEF661 CRC64;

  Query Match             17.8%;  Score 265.5;  DB 1;  Length 415;
  Best Local Similarity   30.9%;  Pred. No. 1.4e-13;
  Matches   72;  Conservative   24;  Mismatches   88;  Indels   49;  Gaps   10;

Qy         20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGEREEEARAC 76
              |::|||| ||   | |   | |  ||   | : ||:|   : || |::: |   ||   |
Db         59 CSRCPPGEFVFAVCSRSQDTVCKTCPHNSYNEHWNHLSTCQLCRPCDIVLG--FEEVAPC 116
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Qy         77 HATHNRACRCRTGFFAHAGFCL----EHASCPPGAGVIA-PGTPSQNT--------QCQP 123
               :     |||: |       |:    |   |     |:  ||| :: |         | |
Db        117 TSDRKAECRCQPGM-----SCVYLDNECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVP 171

Qy        124 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 183
              | || |  :||   :||||  |   ||    ||:|  ||:|        :   |||
Db        172 CKPGHFQNTSSPRARCQPHTRCEIQGLVEAAPGTSYSDTICK-------NPPEPGAMLLL 224

Qy        184 RAVIDFVAF-------------QDISIKRLQRLLQALEAPEGWG----PTPRA 219
                ::  | |                  ::|  ||:    |||      | |||
Db        225 AILLSLVLFLLFTTVLACAWMRHPSLCRKLGTLLK--RHPEGEESPPCPAPRA 275


RESULT 11
CRMB_VARV
ID   CRMB_VARV      STANDARD;      PRT;   349 AA.
AC   P34015; Q85407; Q89098; Q89118;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   CRMB OR G2R OR G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=India-1967 / Isolate Ind3;
RX   MEDLINE=93202281; PubMed=8384129;
RA   Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bangladesh-1975;
RX   MEDLINE=94088747; PubMed=8264798;
RA   Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA   Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA   Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA   Venter C.J.;
RT   "Potential virulence determinants in terminal regions of variola
RT   smallpox virus genome.";
RL   Nature 366:748-751(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966, and Somalia-1977;
RA   Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA   Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966;
RX   MEDLINE=20107289; PubMed=10639322;
RA   Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
RA   Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
RA   Esposito J.J.;
RT   "Alastrim smallpox variola minor virus genome DNA sequences.";
RL   Virology 266:361-386(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
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CC   -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   EMBL; L22579; AAA60933.1; -.
DR   EMBL; U18339; AAA69407.1; -.
DR   EMBL; U18341; AAA69467.1; -.
DR   EMBL; Y16780; CAB54798.1; -.
DR   EMBL; U88146; AAB94371.1; -.
DR   EMBL; U88148; AAB94373.1; -.
DR   EMBL; U88149; AAB94374.1; -.
DR   EMBL; U88152; AAB94377.1; -.
DR   PIR; D36858; D36858.
DR   PIR; D72175; D72175.
DR   PIR; T28623; T28623.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     65       BY SIMILARITY.
FT   DISULFID     68     83       BY SIMILARITY.
FT   DISULFID     86    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    215    215       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      17     17       MISSING (IN STRAINS BANGLADESH-1975 AND
FT                                CHIMP 9-4).
FT   VARIANT     160    160       H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT                                1966 AND SOMALIA-1977).
FT   VARIANT     165    165       A -> T (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
FT   VARIANT     182    182       E -> K (IN STRAIN SOMALIA-1977).
FT   VARIANT     274    274       A -> E (IN STRAIN SOMALIA-1977).
FT   VARIANT     335    335       N -> D (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
FT   VARIANT     339    339       P -> L (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
SQ   SEQUENCE   349 AA;  38189 MW;  D45D40B5C6E780EF CRC64;

  Query Match             17.4%;  Score 260;  DB 1;  Length 349;
  Best Local Similarity   32.2%;  Pred. No. 3.1e-13;
  Matches   59;  Conservative   26;  Mismatches   90;  Indels    8;  Gaps    3;

Qy          5 PTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCN 63
              |    :| |     | |  |||||:  | |   : | | ||    :|   |:|  |  ||
Db         28 PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCN 87

Qy         64 VLCGEREEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQ 117
                |   : | |:|: |||| | |  |::      :    |:    |  | || :  |
Db         88 GRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSVG 146

Qy        118 NTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
              :  | ||  ||:| : ||:::|:|  | |   : : :     :|| ||  |   ||  :
```

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Db         147 DVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVEITLYPVNDTSCTRTTTTGLSESIL 206

Qy         178 GAE 180
                :|
Db         207 TSE 209


RESULT 12
CRMB_CAMPS
ID   CRMB_CAMPS     STANDARD;      PRT;   349 AA.
AC   Q8UYA7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
OS   Camelpox virus (strain CMS), and
OS   Camelpox virus (strain M-96).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=203172, 203173;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CMS;
RX   PubMed=11907336;
RA   Gubser C., Smith G.L.;
RT   "The sequence of camelpox virus shows it is most closely related to
RT   variola virus, the cause of smallpox.";
RL   J. Gen. Virol. 83:855-872(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M-96;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA   Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT   "The genome of camelpox virus.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AY009089; AAG37456.1; -.
DR   EMBL; AY009089; AAG37718.1; -.
DR   EMBL; AF438165; AAL73920.1; -.
DR   EMBL; AF438165; AAL73917.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     65       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     65       BY SIMILARITY.
FT   DISULFID     68     83       BY SIMILARITY.
FT   DISULFID     86    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   349 AA;  38064 MW;  EA412AF991E087F3 CRC64;

  Query Match             17.3%;  Score 257.5;  DB 1;  Length 349;
  Best Local Similarity   32.0%;  Pred. No. 4.9e-13;
  Matches   54;  Conservative   28;  Mismatches   80;  Indels    7;  Gaps    2;

Qy          18 LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACH 77
               | |  |||||:  | |   : | | ||    :|   |:|  |  ||  |   : | |:|:
Db          42 LCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCN 101

Qy          78 ATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSA 131
                |||| | |  |::      :    |:    |  | || :  | : :  | ||  ||:|
Db         102 TTHNRICECSPGYYCILKGSSGCKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSR 160

Qy         132 SSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
               : ||:::|:|  : |   : : :     :|| ||  |   :|  :  :|
Db         161 TVSSADKCEPVPSNTFNYIDVEINLYPVNDTSCTRTTTTGISESISTSE 209


RESULT 13
CRMB_COWPX
ID   CRMB_COWPX     STANDARD;      PRT;   351 AA.
AC   O73559;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR D2L) AND (CRMB2 OR H4R).
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90 / Grishak;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "The genomic sequence analysis of the left and right species-specific
RT   terminal region of a cowpox virus strain reveals unique sequences and
RT   a cluster of intact ORFs for immunomodulatory and host range
RT   proteins.";
RL   Virology 243:432-460(1998).
RN   [2]
RP   FUNCTION.
RC   STRAIN=Brighton red;
RX   MEDLINE=94378510; PubMed=8091665;
RA   Hu F.Q., Smith C.A., Pickup D.J.;
RT   "Cowpox virus contains two copies of an early gene encoding a soluble
RT   secreted form of the type II TNF receptor.";
RL   Virology 204:343-356(1994).
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Y11842; CAA72578.1; -.
DR   EMBL; Y15035; CAA75306.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
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DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    351       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     67       TNFR-CYS 1.
FT   REPEAT       69    110       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     67       BY SIMILARITY.
FT   DISULFID     70     85       BY SIMILARITY.
FT   DISULFID     88    102       BY SIMILARITY.
FT   DISULFID     92    110       BY SIMILARITY.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   351 AA;  38253 MW;  57CAE73EF4E5D7C7 CRC64;

  Query Match             17.1%;  Score 254.5;  DB 1;  Length 351;
  Best Local Similarity   32.2%;  Pred. No. 8.4e-13;
  Matches   55;  Conservative   29;  Mismatches   78;  Indels    9;  Gaps    3;

Qy          18 LVCAQCPPGTFVQRPC--RRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARA 75
               | |  |||||:  | |  : :: | | ||    :|   |:|  |  ||  |   : | |:
Db          42 LCCLSCPPGTYASRLCDSKTNTNTQCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVETRS 101

Qy          76 CHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
               |: |||| | |  |::      :    |:    |  | || :  | : :  | ||  ||:
Db         102 CNTTHNRICECAPGYYCLLKGSSGCKACVSQTKCGIGYGV-SGHTSTGDVVCSPCGLGTY 160

Qy         130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
               | : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db         161 SHTVSSADKCEPVPSNTFNYIDVEINLYPVNDTSCTRTTTTGLSESISTSE 211


RESULT 14
TR14_HUMAN
ID   TR14_HUMAN     STANDARD;      PRT;   283 AA.
AC   Q92956; Q8WXR1; Q96J31; Q9UM65;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 14 precursor
DE   (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE   (TR2).
GN   TNFRSF14 OR HVEM OR HVEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervical adenocarcinoma;
RX   MEDLINE=97053782; PubMed=8898196;
RA   Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT   "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT   the TNF/NGF receptor family.";
RL   Cell 87:427-436(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97306336; PubMed=9162061;
RA   Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA   Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA   Porter T.G., Truneh A., Young P.R.;
RT   "A newly identified member of the tumor necrosis factor receptor
RT   superfamily with a wide tissue distribution and involvement in
RT   lymphocyte activation.";
RL   J. Biol. Chem. 272:14272-14276(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Zhang W., Wan T., Cao X.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
RX   MEDLINE=21629477; PubMed=11756979;
RA   Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,
RA   Spear P.G.;
RT   "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT   Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL   J. Infect. Dis. 185:36-44(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   INTERACTION WITH TRAF2 AND TRAF5.
RX   PubMed=9153189;
RA   Hsu H., Solovyev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
RT   "ATAR, a novel tumor necrosis factor receptor family member, signals
RT   through TRAF2 and TRAF5.";
RL   J. Biol. Chem. 272:13471-13474(1997).
RN   [7]
RP   INTERACTION WITH TRAF3 AND TRAF5.
RX   PubMed=9162022;
RA   Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
RA   Ashkenazi A.;
RT   "Herpesvirus entry mediator, a member of the tumor necrosis factor
RT   receptor (TNFR) family, interacts with members of the TNFR-associated
RT   factor family and activates the transcription factors NF-kappaB and
RT   AP-1.";
RL   J. Biol. Chem. 272:14029-14032(1997).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX   MEDLINE=21403268; PubMed=11511370;
RA   Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
RA   Eisenberg R.J., Wiley D.C.;
RT   "Herpes simplex virus glycoprotein D bound to the human receptor
RT   HveA.";
RL   Mol. Cell 8:169-179(2001).
CC   -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
CC       an important role in HSV pathogenesis because it enhanced the
CC       entry of several wildtype HSV strains of both serotypes into CHO
CC       cells, and mediated HSV entry into activated human T cells.
CC   -!- SUBUNIT: INTERACTS WITH TRAF2, TRAF3 AND TRAF5.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC       IN LUNG, SPLEEN, AND THYMUS.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; U70321; AAB58354.1; -.
DR   EMBL; U81232; AAD00505.1; -.
DR   EMBL; AF153978; AAF75588.1; -.
DR   EMBL; AF373877; AAL47717.1; -.
DR   EMBL; AF373878; AAL47718.1; -.
DR   EMBL; BC002794; AAH02794.1; -.
DR   PDB; 1JMA; 26-SEP-01.
DR   Genew; HGNC:11912; TNFRSF14.
DR   MIM; 602746; -.
DR   GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW   3D-structure.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    283       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 14.
FT   DOMAIN       39    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    223       POTENTIAL.
FT   DOMAIN      224    283       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     75       TNFR-CYS 1.
FT   REPEAT       78    119       TNFR-CYS 2.
FT   REPEAT      121    162       TNFR-CYS 3.
FT   DISULFID     42     53
FT   DISULFID     54     67
FT   DISULFID     57     75
FT   DISULFID     78     93
FT   DISULFID     96    111
FT   DISULFID     99    119
FT   DISULFID    121    138
FT   DISULFID    127    135
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      17     17       K -> R (IN dbSNP:4870).
FT                                /FTId=VAR_013007.
FT   VARIANT     241    241       V -> I.
FT                                /FTId=VAR_013440.
FT   TURN         44     45
FT   STRAND       46     46
FT   STRAND       49     49
FT   TURN         50     51
FT   STRAND       52     52
FT   STRAND       55     55
FT   STRAND       57     57
FT   TURN         59     60
FT   STRAND       61     65
FT   STRAND       74     77
FT   TURN         80     81
FT   STRAND       82     83
FT   STRAND       88     88
FT   STRAND       94     95
FT   TURN        101    104
FT   STRAND      105    109
FT   STRAND      118    121
FT   TURN        123    124
FT   STRAND      125    129
FT   STRAND      137    140
SQ   SEQUENCE   283 AA;  30392 MW;  46CE13C2C70242C1 CRC64;

  Query Match             16.4%;  Score 244;  DB 1;  Length 283;
  Best Local Similarity   37.3%;  Pred. No. 4.3e-12;
  Matches   56;  Conservative   14;  Mismatches   68;  Indels   12;  Gaps    4;

Qy         20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLER---CRYCNVLCGEREEEARAC 76
              | :| ||  |:  |   : | | ||||  |    | | :   |: |:   | |   :| |
Db         54 CPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLR--ASRNC 111
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Qy         77 HATHNRACRCRTGFFA------HAGFCLEHASCPPGAGVIAPGTPSQNTCQCPCPPGTFS 130
                | |  | |  | |       |   |  :|:  ||  |   || ||:| || |||||||
Db        112 SRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS 171

Qy        131 ASSSSSEQCQPHRNCTALGLALNVPGSSSH 160
                : : |:||    |: |        ||||
Db        172 -PNGTLEECQHQTKCSWLVTKAGAGTSSSH 200

RESULT 15
TR11_HUMAN
ID   TR11_HUMAN     STANDARD;      PRT;   616 AA.
AC   Q9Y6Q6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11A precursor
DE   (Receptor activator of NF-KB) (Osteoclast differentiation factor
DE   receptor) (ODFR).
GN   TNFRSF11A OR RANK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dendritic cell;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=99097247; PubMed=9878548;
RA   Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA   Morinaga T., Higashio K.;
RT   "RANK is the essential signaling receptor for osteoclast
RT   differentiation factor in osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 253:395-400(1998).
RN   [3]
RP   INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.
RX   PubMed=9774460;
RA   Wong B.R., Josien R., Lee S.Y., Vologodskaia M., Steinman R.M.,
RA   Choi Y.;
RT   "The TRAF family of signal transducers mediates NF-kappaB activation
RT   by the TRANCE receptor.";
RL   J. Biol. Chem. 273:28355-28359(1998).
RN   [4]
RP   VARIANT FEO 16-LEU--LEU-21 DUPL, VARIANT PDB2 13-ALA--LEU-21 DUPL, AND
RP   VARIANT VAL-192.
RX   MEDLINE=20082806; PubMed=10615125;
RA   Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA   Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA   Anderson D.M.;
RT   "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT   familial expansile osteolysis.";
RL   Nat. Genet. 24:45-48(2000).
CC   -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for
CC       RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC       interactions between T-cells and dendritic cells.
CC   -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC       SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC       GLAND.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE
CC       OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
CC       CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
CC       OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
CC       ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
```

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CC       LOSS OF DENTITION.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET
CC       DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT
CC       IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO.
CC       UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE
CC       AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF018253; AAB86809.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:11908; TNFRSF11A.
DR   MIM; 603499; -.
DR   MIM; 174810; -.
DR   MIM; 602080; -.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW   Disease mutation; Deafness.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    616       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11A.
FT   DOMAIN       30    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    233       POTENTIAL.
FT   DOMAIN      234    616       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       34     68       TNFR-CYS 1.
FT   REPEAT       71    112       TNFR-CYS 2.
FT   REPEAT      114    151       TNFR-CYS 3.
FT   REPEAT      154    194       TNFR-CYS 4.
FT   DISULFID     34     46       BY SIMILARITY.
FT   DISULFID     47     60       BY SIMILARITY.
FT   DISULFID     50     68       BY SIMILARITY.
FT   DISULFID     71     86       BY SIMILARITY.
FT   DISULFID     92    112       BY SIMILARITY.
FT   DISULFID    114    127       BY SIMILARITY.
FT   DISULFID    133    151       BY SIMILARITY.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      21     21       L -> LALLLLCALL (IN PDB2).
FT                                /FTId=VAR_011516.
FT   VARIANT      21     21       L -> LLLCALL (IN FEO).
FT                                /FTId=VAR_011517.
FT   VARIANT     192    192       A -> V.
FT                                /FTId=VAR_011518.
SQ   SEQUENCE   616 AA;  66033 MW;  E3DE9A7A08196F81 CRC64;

  Query Match             15.8%;  Score 235.5;  DB 1;  Length 616;
  Best Local Similarity   31.3%;  Pred. No. 4.5e-11;
  Matches   52;  Conservative   26;  Mismatches   77;  Indels   11;  Gaps    4;

Qy         20 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 76
              | :| || ::   |   | : | || |  |   ||  ::|   : |:   |:      |
Db         47 CNKCEPGKYMSSKCTTTSDSVCLPCGPDEYLDSWNEEDKCLLHKVCDT--GKALVAVVAG 104

Qy         77 HATHNRACRCRTGFF--AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSS 134
              ::|  | | |  |:        |  :  | || |   |   :::| |:||  | || : |
Db        105 NSTTPRRCACTAGYHWSQDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFS 164

Qy        135 SSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              |:::|:|  ||| ||  :   |:   | :|:|     |  | |  |
Db        165 STDKCRPWTNCTFLGKRVEHHGTEKSDAVCSS----SLPARKPPNE 206

Search completed: December  3, 2003, 13:13:11
Job time : 18 secs
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:         December  3, 2003, 13:08:01 ; Search time 41 Seconds
                                         (without alignments)
                                         1705.665 Million cell updates/sec

Title:          US-10-069-385-1
Perfect score:  1491
Sequence:       1 VAETPTYPWRDAETGERLVC..........RVARMPGLERSVRERFLPVH 271

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:      830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_23:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10:  sp_plant:*
                11:  sp_rodent:*
                12:  sp_virus:*
                13:  sp_vertebrate:*
                14:  sp_unclassified:*
                15:  sp_rvirus:*
                16:  sp_bacteriap:*
                17:  sp_archeap:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
                %
Result          Query
  No.   Score   Match Length DB  ID                          Description
 ------------------------------------------------------------------------
    1   499.5   33.5    285  13  Q90W71                  Q90w71 oncorhynchu
    2   486.5   32.6    285  13  Q90YS6                  Q90ys6 oncorhynchu
    3     395   26.5    302  13  Q9PUS0                  Q9pus0 salvelinus
    4   333.5   22.4    459  11  Q62327                  Q62327 mus musculu
    5     327   21.9    482  11  O88734                  O88734 mus musculu
    6   317.5   21.3    457  4   Q8IVS6                 Q8ivs6 homo sapien
    7   313.5   21.0    433  11  Q91ZM6                  Q91zm6 rattus norv
    8     287   19.2    651  13  Q98SM6                  Q98sm6 gallus gall
    9     275   18.4    348  12  O57108                  O57108 monkeypox v
   10     275   18.4    348  12  O57277                  O57277 monkeypox v
   11     275   18.4    348  12  O57103                  O57103 monkeypox v
   12   270.5   18.1    349  12  O57100                  O57100 monkeypox v
   13   268.5   18.0    349  12  O57101                  O57101 monkeypox v
   14   268.5   18.0    349  12  O57102                  O57102 monkeypox v
   15   268.5   18.0    349  12  O57291                  O57291 monkeypox v
   16   267.5   17.9    349  12  O57099                  O57099 monkeypox v
   17     260   17.4    348  12  O57112                  O57112 variola vir
   18     260   17.4    349  12  O57111                  O57111 variola vir
   19     260   17.4    349  12  O57110                  O57110 variola vir
   20     260   17.4    350  12  O57116                  O57116 cowpox viru
   21     259   17.4    360  12  O57118                  O57118 cowpox viru
   22   258.5   17.3    355  12  Q85308                  Q85308 cowpox viru
   23   257.5   17.3    326  12  O57120                  O57120 cowpox viru
   24   257.5   17.3    349  12  O57098                  O57098 camelpox vi
   25   257.5   17.3    349  12  O57284                  O57284 camelpox vi
   26   254.5   17.1    326  12  O57122                  O57122 cowpox viru
   27   253.5   17.0    349  12  O57097                  O57097 camelpox vi
   28   253.5   17.0    349  12  O57305                  O57305 cowpox viru
   29   253.5   17.0    351  12  O57117                  O57117 cowpox viru
   30     252   16.9    349  12  O57109                  O57109 variola vir
   31     251   16.8    347  12  O57119                  O57119 cowpox viru
   32   249.5   16.7    347  12  O57115                  O57115 cowpox viru
   33   248.5  .16.7    351  12  O57121                  O57121 cowpox viru
   34   245.5   16.5    350  12  O57123                  O57123 cowpox viru
   35     244   16.4    283  6   Q9XSZ8                 Q9xsz8 cercopithec
   36   230.5   15.5    276  13  Q9DDD2                  Q9ddd2 gallus gall
   37     227   15.2    278  6   Q8SQ34                 Q8sq34 sus scrofa
   38     224   15.0    573  11  Q8BZU6                  Q8bzu6 mus musculu
   39   219.5   14.7    277  6   Q8WMQ2                 Q8wmq2 ovis aries
   40   203.5   13.6    267  6   O02764                 O02764 oryctolagus
   41     203   13.6    289  11  Q8K2X6                  Q8k2x6 mus musculu
   42     202   13.5    132  13  Q90Y18                  Q90y18 salvelinus
   43     200   13.4    167  12  Q9DJL2                  Q9djl2 cowpox viru
   44     200   13.4    169  11  Q9JKE0                  Q9jke0 rattus norv
   45     199   13.3    167  12  Q8UYL3                  Q8uyl3 vaccinia vi

                               ALIGNMENTS

RESULT 1
Q90W71
ID   Q90W71      PRELIMINARY;      PRT;   285 AA.
AC   Q90W71;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative decoy receptor 3 protein.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leukocyte;
RA   Pleguezuelos O., Secombes C.J.;
RT   "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ315137; CAC43329.1; -.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   285 AA;  31642 MW;  FB75CFFC1E391AD0 CRC64;

  Query Match             33.5%;  Score 499.5;  DB 13;  Length 285;
  Best Local Similarity   37.1%;  Pred. No. 1.3e-36;
  Matches   99;  Conservative   41;  Mismatches  116;  Indels   11;  Gaps    4;

Qy          2 AETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY 61
              | |||| |||   ||: | |   | |||:: : | :|   : |||||   |||: |||:|||:|
Db         26 AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGPCPKSHYTEIWNYIERCQY 85

Qy         62 CNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121
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                 ||   |    | |:  |    ||| | |: ||:   | |  |   |||| |||: ||    : :|
Db          86 CNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKC 145

Qy         122 QPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
                :||| | ||| ||| : ||      |     |      :||:  :|  |::||      |     |
Db         146 EPCPVGFFSAVSSSRKACQKFSVCPPGG--TTIPGNDMNDVYCSACTNG--SRTHEGEAI 201

Qy         182 CERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDG 241
               |:  :::|:: | :: :: :||:  |      |     |        | | | : :       |
Db         202 CDGELMEFLSLQILTPRKDKRLVAVLRRSAGKATT----NNATVLDLLKTIKNKAGKH-- 255

Qy         242 ALLVRLLQALRVARMPGLERSVRERFL 268
                   :::     |  |:  |    | : ||
Db         256 -FAIQMRDILNTDRLLHLRTKVNKWFL 281


RESULT 2
Q90YS6
ID   Q90YS6      PRELIMINARY;      PRT;   285 AA.
AC   Q90YS6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TNF decoy receptor.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT   "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT   with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT   fragments containing AU-rich elements.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF401631; AAK91758.1; -.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   285 AA;  31795 MW;  5E3BD1B6EFC6BABC CRC64;

  Query Match             32.6%;  Score 486.5;  DB 13;  Length 285;
  Best Local Similarity   36.3%;  Pred. No. 1.9e-35;
  Matches   97;  Conservative   41;  Mismatches  118;  Indels   11;  Gaps    4;

Qy           2 AETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRY 61
               | |||| |||   ||: |  |  | |||:: : | :|   : |||||  |||: |||:|||:|
Db          26 AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGPCPKSHYTEIWNYIERCQY 85

Qy          62 CNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQC 121
               ||   |   | |:  |    ||| | |: ||:   | |  |   |||| |||: ||    : :|
Db          86 CNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKC 145

Qy         122 QPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 181
               :||| | ||| ||| : ||      |            :||:  :|  |::|      |     |
Db         146 EPCPVGFFSAVSSSRKACQKFSVCPP--GRTTIPGNDMNDVYCSACRNG--SRTHEGQAI 201

Qy         182 CERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQDG 241
               |:  :::|:: | :: :: :||:  |      |     |        | | | : :       |
Db         202 CDGELMEFLSLQILTPRKDKRLVAVLRRSAGKATT----NNATVLDLLKTIKNKAGKH-- 255

Qy         242 ALLVRLLQALRVARMPGLERSVRERFL 268
                   :::     |  |:  |    | : ||
Db         256 -FAIQMRDILNTDRLLHLRTKVNKWFL 281

RESULT 3
Q9PUS0
ID   Q9PUS0      PRELIMINARY;      PRT;   302 AA.
AC   Q9PUS0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Decoy TNF receptor.
OS   Salvelinus fontinalis (Brook trout) (Brook char).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX   NCBI_TaxID=8038;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20111091; PubMed=10642582;
RA   Bobe J., Goetz F.W.;
RT   "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT   the brook trout (Salvelinus fontinalis) ovary at the completion of
RT   ovulation.";
RL   Biol. Reprod. 62:420-426(2000).
DR   EMBL; AF156738; AAD56428.1; -.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   302 AA;  34037 MW;  E44C73477F05C3DF CRC64;

  Query Match             26.5%;  Score 395;  DB 13;  Length 302;
  Best Local Similarity   34.3%;  Pred. No. 2.8e-27;
  Matches   82;  Conservative   44;  Mismatches  101;  Indels   12;  Gaps    7;

Qy           6 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 65
               |:    |    :|   :||  :|||||:::  ||           :  |   ||     ||:|||:: :|   |: :
Db          22 TFKNDDRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-M 80

Qy          66 CGEREEEARACHATHNRACRCRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSQNTQCQP 123
               | |  :     :  |   ::|    | |:  |::  :    :   |::|   ||||          ||| |:|:|
Db          81 CAENQVVKQECSPSNNCECECKEGYYFNKKYEACIKHKECPPGYGANTTGTPHQDTECVQ 140

Qy         124 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 183
               |   | :|  ||:    |       ||     || : :  |      |:||| ||   :  |  ||    |||
Db         141 CQAGFYSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCASC--YDLKTR-DGAEYLH 197

Qy         184 RAVIDFV--AFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240
                     :  |        | : |||::||  |:  |:  |   |   |   |:   :  ||  | : : : |
Db         198 EILPTFFIQLHQTMGIKRMRRL--AMRLPQEGGKKPLIG--AVMKRNRRGLHDFMNSWD 252


RESULT 4
Q62327
ID   Q62327      PRELIMINARY;      PRT;   459 AA.
AC   Q62327;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Murine tumour necrosis factor receptor 2 protein (Fragment).
GN   TNFRSF1B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT   linked to autoimmune diabetes in NOD mice.";
RL   Genomics 0:0-0(0).
```

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RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RX   MEDLINE=95178848; PubMed=7873884;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Allelic variation of the type 2 tumor necrosis factor receptor
RT   gene.";
RL   Mamm. Genome 5:726-727(1994).
DR   EMBL; X76401; CAA53981.1; -.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   VARIANT      87     87       S -> T.
FT   VARIANT      93     93       T -> I.
FT   VARIANT     268    268       F -> I.
FT   VARIANT     345    345       S -> F.
FT   VARIANT     421    421       Y -> C.
SQ   SEQUENCE   459 AA;  48686 MW;  6C51D2CF1C4626DF CRC64;

  Query Match             22.4%;  Score 333.5;  DB 11;  Length 459;
  Best Local Similarity   29.7%;  Pred. No. 1.3e-21;
  Matches   81;  Conservative   43;  Mismatches  110;  Indels   39;  Gaps    9;

Qy         17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
              :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db         37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC 96

Qy         77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                  || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db         97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156

Qy        130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 185
              | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db        157 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 212

Qy        186 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 240
               :|    |:    :   :| :|      | ||       |  :| : |   :| |
Db        213 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257

Qy        241 GALLVRLLQAL----RVARMPGLERSVRERFLP 269
              | |:: |:       |  :   |:|  :   :|
Db        258 GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 290

RESULT 5
O88734
ID   O88734      PRELIMINARY;      PRT;   482 AA.
AC   O88734;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P80 TNF-alpha receptor.
GN   TNFR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98414512; PubMed=9740674;
RA   Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT   "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT   and Characterization of the two Transcripts.";
RL   Genomics 52:79-98(1998).
DR   EMBL; Y14619; CAA74969.1; -.
DR   EMBL; Y14620; CAA74969.1; JOINED.
DR   EMBL; Y14621; CAA74969.1; JOINED.
DR   EMBL; Y14622; CAA74969.1; JOINED.
DR   EMBL; Y14623; CAA74969.1; JOINED.
DR   EMBL; Y14679; CAA74969.1; JOINED.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
SQ   SEQUENCE   482 AA;  51106 MW;  F6C15046B48FF83C CRC64;

  Query Match             21.9%;  Score 327;  DB 11;  Length 482;
  Best Local Similarity   29.3%;  Pred. No. 5.3e-21;
  Matches   82;  Conservative   43;  Mismatches  109;  Indels   46;  Gaps   10;

Qy         17 RLVCAQCPPGTFVQRPCRR-------DSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGER 69
              :: ||:|||| :|:  | :       || | |  |    ||| ||    |  |:  |
Db         52 QMCCAKCPPGQYVKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTD 111

Qy         70 EEEARACHATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQ 122
              : | |||    || | |  | :     |:|    |:  : | || || :   |: |  |:
Db        112 QVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCK 171

Qy        123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPG 178
               | ||||| ::||:: |:||| |: |     :||::| | :|     : :  | :  |
Db        172 ACAPGTFSDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQ 227

Qy        179 AEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLT 233
               |      :|    |:    :   :| :|      | ||       |  :| : |   :|
Db        228 PEPTRSQPLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVT 277

Qy        234 ELLGAQDGALLVRLLQAL----RVARMPGLERSVRERFLP 269
               |     | |:: |:       |  :   |:|  :   :|
Db        278 SL-----GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 312

RESULT 6
Q8IVS6
ID   Q8IVS6      PRELIMINARY;      PRT;   457 AA.
AC   Q8IVS6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to tumor necrosis factor receptor superfamily, member 1B
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC042167; AAH42167.1; -.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   457 AA;  48120 MW;  1B634BBF1F5D77AC CRC64;

  Query Match             21.3%;  Score 317.5;  DB 4;  Length 457;
  Best Local Similarity   30.3%;  Pred. No. 3.5e-20;
  Matches   80;  Conservative   39;  Mismatches  108;  Indels   37;  Gaps    9;

Qy         25 PGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRAC 84
              ||   :  | : | | |  |    ||| ||::  |  |   |   : | :||    || |
Db         55 PGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRIC 114

Qy         85 RCRTGFFAHAG------FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQ 138
               || |::           |     | || ||  ||| : :  |:|| ||||| ::||::
Db        115 TCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 174

Qy        139 CQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIK 198
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              |:||: |  :     :||::| | :||| :  |  :  |||    : |           :
Db        175 CRPHQICNVVA----IPGNASMDAVCTSTS--PTRSMAPGAVHLPQPV-------STRSQ 221

Qy        199 RLQRLLQALEAPE-----GWGPTPRA----GRAALQLKLRRRLTELLGAQDGALLVRLLQ 249
                    :   ||        ||:| |    |  || : |   :| |     | ::  ::
Db        222 HTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVN 276

Qy        250 AL---RVARMP-GLERSVRERFLP 269
               :   :| : |  |:|  :   ||
Db        277 CVIMTQVKKKPLCLQREAKVPHLP 300


RESULT 7
Q91ZM6
ID   Q91ZM6      PRELIMINARY;      PRT;   433 AA.
AC   Q91ZM6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor type II (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT   "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT   capillary endothelial cells and participate in TNF-alpha transport
RT   through the blood-brain barrier.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF420214; AAL16021.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     433    433
SQ   SEQUENCE   433 AA;  45723 MW;  75736D835E72CA4A CRC64;

  Query Match             21.0%;  Score 313.5;  DB 11;  Length 433;
  Best Local Similarity   35.1%;  Pred. No. 7.6e-20;
  Matches   59;  Conservative   29;  Mismatches   67;  Indels   13;  Gaps    4;

Qy         17 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 76
              :: ||:|||| : :  | : | | |  |    :|| ||:|  |  |:  | : : |   |
Db         32 QMCCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQVETHNC 91

Qy         77 HATHNRACRCRTGFFA----HAG---FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 129
                  || | |    :     |:|    |:: : | || ||    | : |  |  | ||||
Db         92 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF 151

Qy        130 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 177
              | ::||:: |:||| |: |     :||::| | :| | :  |  : ||
Db        152 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCASES--PTPSAVP 193


RESULT 8
Q98SM6
ID   Q98SM6      PRELIMINARY;      PRT;   651 AA.
AC   Q98SM6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Death receptor 6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bridgham J.T., Johnson A.L.;
RT   "Expression of DR6 in the ovary.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349908; AAK29666.2; -.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   651 AA;  71003 MW;  BDC95A600DAB2C2A CRC64;

  Query Match             19.2%;  Score 287;  DB 13;  Length 651;
  Best Local Similarity   33.5%;  Pred. No. 2.7e-17;
  Matches   54;  Conservative   27;  Mismatches   80;  Indels    0;  Gaps    0;

Qy         11 DAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGERE 70
              |  | : |:| :|| ||:| : | : :   | |||   : :  | :|||  |   |
Db         43 DRATNQELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPM 102

Qy         71 EEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFS 130
               |   | |  :| | | :| |     |: :  || | ||   || ::: :|:||  ||||
Db        103 IEKTHCTALTDRECTCLSGTFQINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162

Qy        131 ASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFP 171
                 ||  :|: : :|    : :  ||:   | :| |    |
Db        163 DVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVCGSPASLP 203


RESULT 9
O57108
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Zaire-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38212 MW;  E555979057DEC91F CRC64;

  Query Match             18.4%;  Score 275;  DB 12;  Length 348;
  Best Local Similarity   33.1%;  Pred. No. 1.6e-16;
  Matches   59;  Conservative   29;  Mismatches   82;  Indels    8;  Gaps    3;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92
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Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              || |||:| : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db        152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTGLSESISTSE 209


RESULT 10
O57277
ID   O57277      PRELIMINARY;      PRT;   348 AA.
AC   O57277;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog (J2R) (J2L).
GN   CRMB OR J2R OR J2L.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1996 /96-17, and ZAIRE-1996 / 96-16;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Zaire-96-I-16;
RX   MEDLINE=21592287; PubMed=11734207;
RA   Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
RA   Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
RA   Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
RA   Sandakhchiev L.S.;
RT   "Human monkeypox and smallpox viruses: genomic comparison.";
RL   FEBS Lett. 509:66-70(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Zaire-96-I-16;
RA   Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
RA   Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
RA   Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88543; AAB94378.1; -.
DR   EMBL; U87841; AAB94358.1; -.
DR   EMBL; AF380138; AAL40648.1; -.
DR   EMBL; AF380138; AAL40460.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  54019521556C2D8F CRC64;

  Query Match             18.4%;  Score 275;  DB 12;  Length 348;
  Best Local Similarity   33.1%;  Pred. No. 1.6e-16;
  Matches   59;  Conservative   29;  Mismatches   82;  Indels    8;  Gaps    3;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              || |||:| : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db        152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTGLSESISTSE 209


RESULT 11
O57103
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Zaire-1979;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38184 MW;  34A5E668B27907B5 CRC64;

  Query Match             18.4%;  Score 275;  DB 12;  Length 348;
  Best Local Similarity   33.1%;  Pred. No. 1.6e-16;
  Matches   59;  Conservative   29;  Mismatches   82;  Indels    8;  Gaps    3;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180
              || |||:| : ||:::|:|  : |   : : :     :|| ||  |   ||  :  :|
Db        152 PCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVNDTSCTRTTTGLSESISTSE 209


RESULT 12
O57100
ID   O57100      PRELIMINARY;      PRT;   349 AA.
AC   O57100;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nigeria-1971;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87844; AAB94361.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
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DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38239 MW;  DF6C280D478F2422 CRC64;

  Query Match             18.1%;  Score 270.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 4.1e-16;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGASGCSTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
              || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db        152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy        180 E 180
              |
Db        210 E 210


RESULT 13
O57101
ID   O57101      PRELIMINARY;      PRT;   349 AA.
AC   O57101;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Zaire-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87845; AAB94362.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38311 MW;  02F65B00CFB858BE CRC64;

  Query Match             18.0%;  Score 268.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 6.2e-16;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
              || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db        152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy        180 E 180
              |
Db        210 E 210


RESULT 14
O57102
ID   O57102      PRELIMINARY;      PRT;   349 AA.
AC   O57102;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Benin-1978;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87846; AAB94363.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38308 MW;  CBD2C949F994C59C CRC64;

  Query Match             18.0%;  Score 268.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 6.2e-16;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGASGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
              || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db        152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy        180 E 180
              |
Db        210 E 210


RESULT 15
O57291
ID   O57291      PRELIMINARY;      PRT;   349 AA.
AC   O57291;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; U88144; AAB94369.1; -.
DR   EMBL; U87842; AAB94359.1; -.
DR   EMBL; U87994; AAB94365.1; -.
DR   EMBL; U87995; AAB94366.1; -.
DR   EMBL; U88143; AAB94368.1; -.
DR   HSSP; Q92956; 1JMA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   349 AA;  38295 MW;  CBD2C949ED2B8E7C CRC64;

  Query Match             18.0%;  Score 268.5;  DB 12;  Length 349;
  Best Local Similarity   32.6%;  Pred. No. 6.2e-16;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels   13;  Gaps    5;

Qy         10 RDAETGER-LVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGE 68
              :| |   | | |  |||||:  | |   : | | ||    :|   |:|: |  ||  |
Db         33 KDNEYRSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHLQACLSCNGRCDS 92

Qy         69 REEEARACHATHNRACRCRTGFF------AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQ 122
               : | |:|: |||| | |  |::      :    |:    |  | || :  | : :  |
Db         93 NQVETRSCNTTHNRICECSPGYYCLLKGASGCRTCISKTKCGIGYGV-SGYTSTGDVICS 151

Qy        123 PCPPGTFSASSSSSEQCQP---HRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGA 179
              || |||:| : ||:::|:|         : : :|:     :|| ||  |   ||  :  :
Db        152 PCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINL--YPVNDTSCTRTTTTGLSESISTS 209

Qy        180 E 180
              |
Db        210 E 210

Search completed: December  3, 2003, 13:14:05
Job time : 43 secs
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